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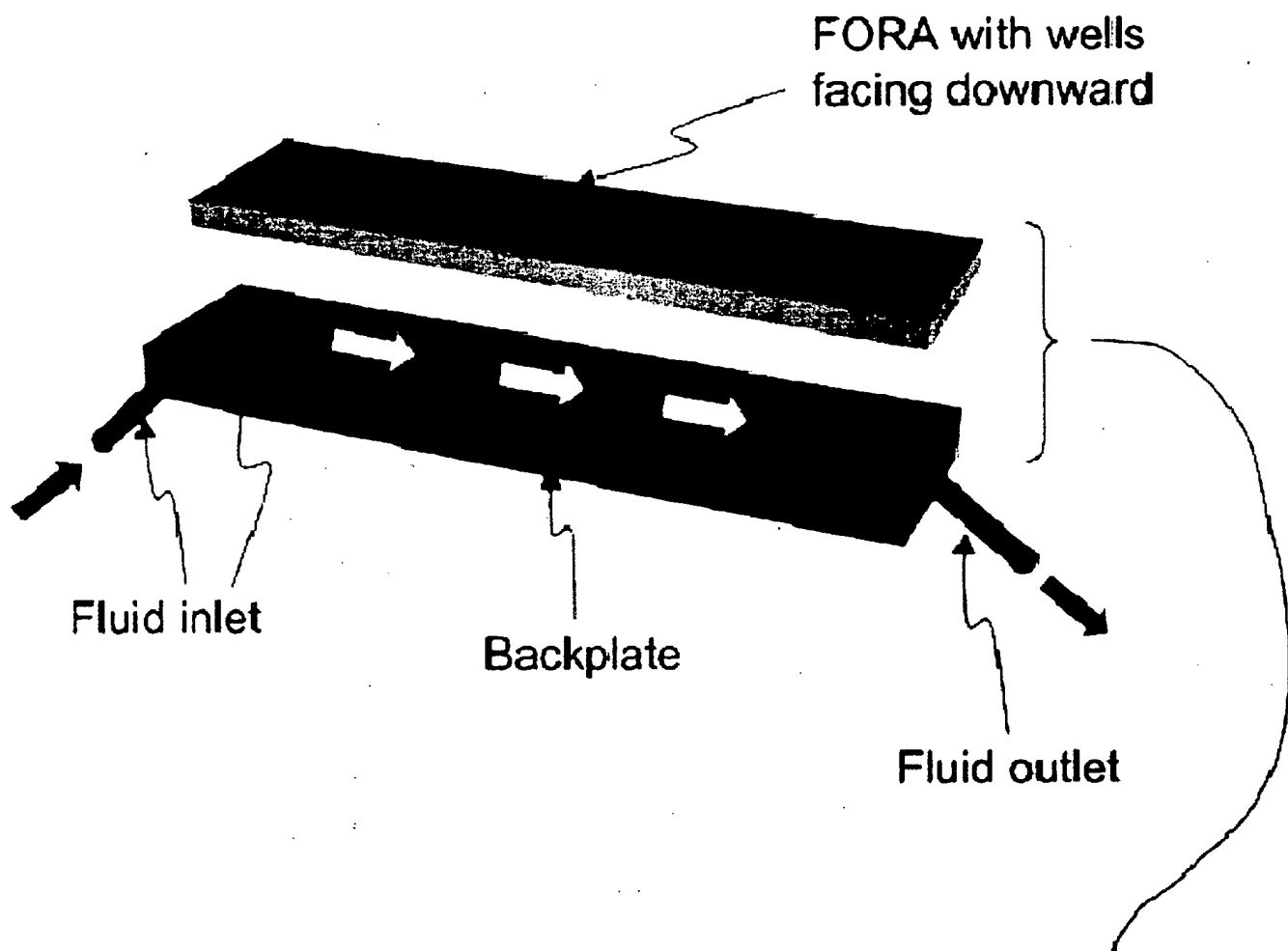
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FORA and back-plate are pressed together with a seal to create a closed flow chamber.

Figure 16

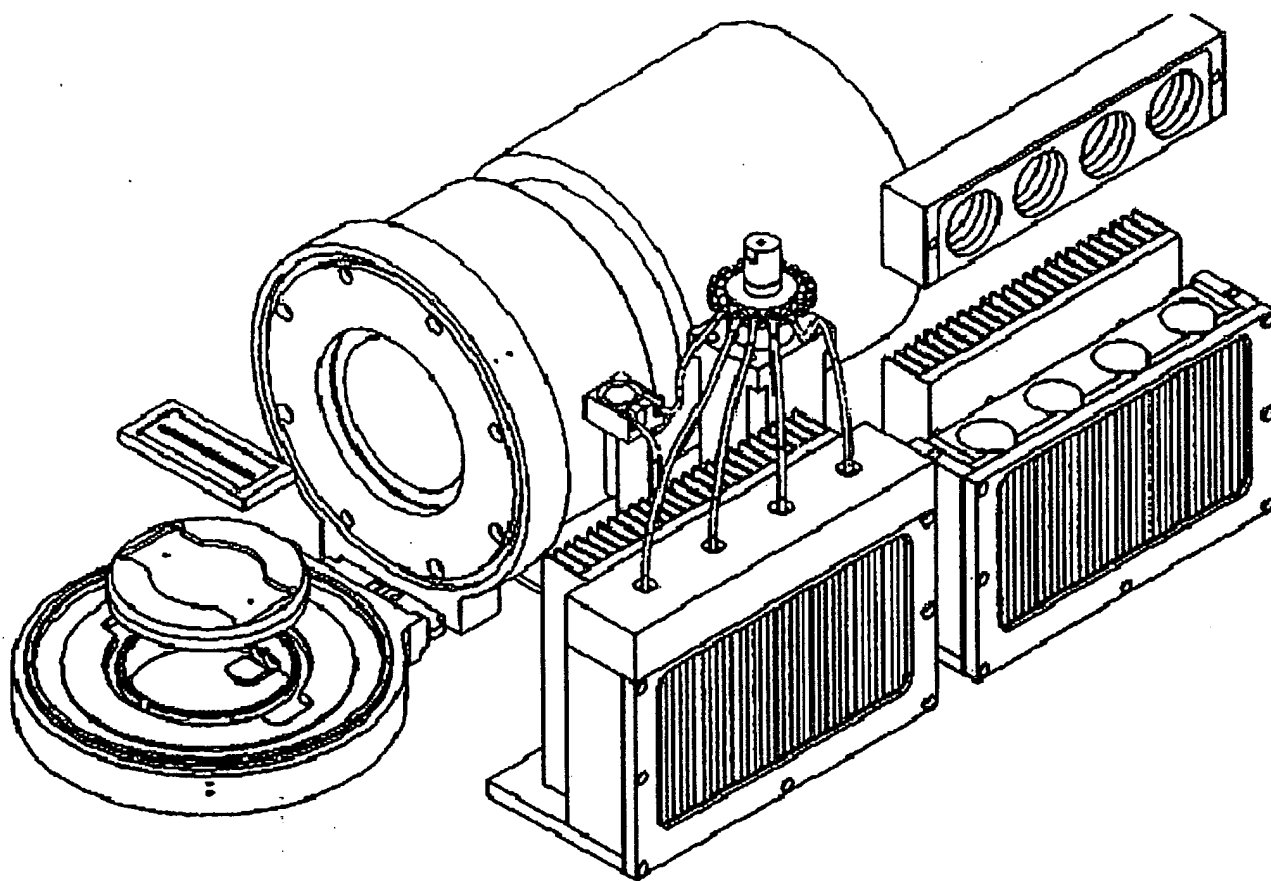


Figure 17

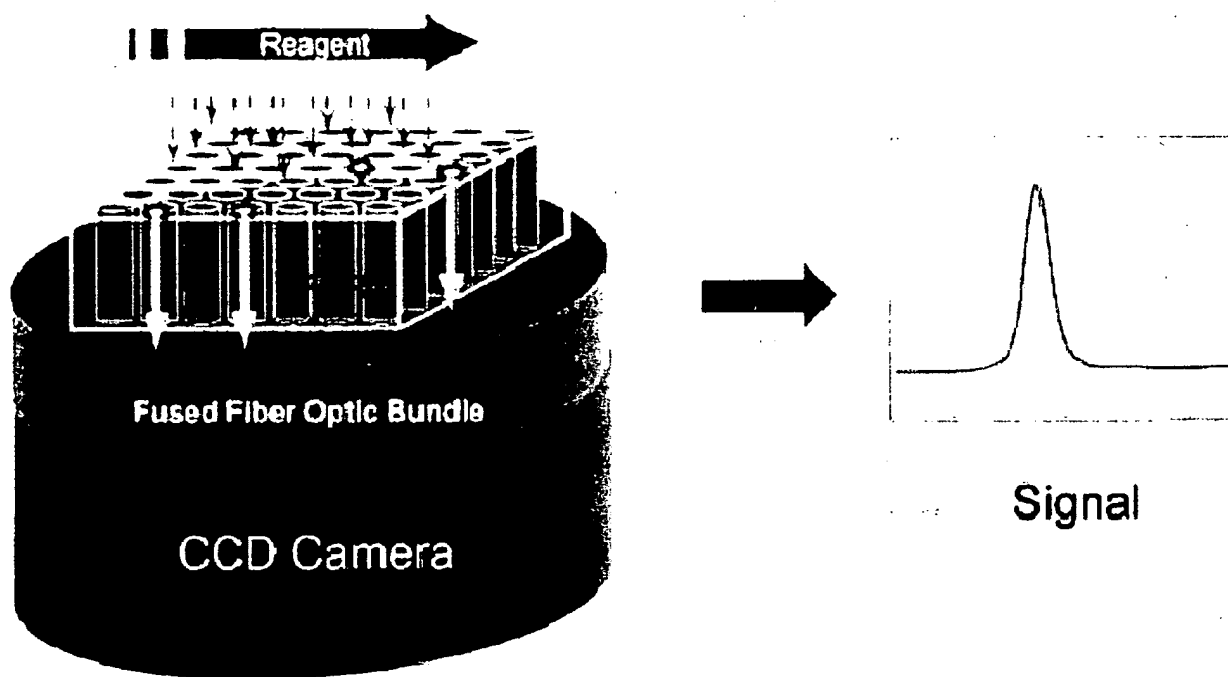
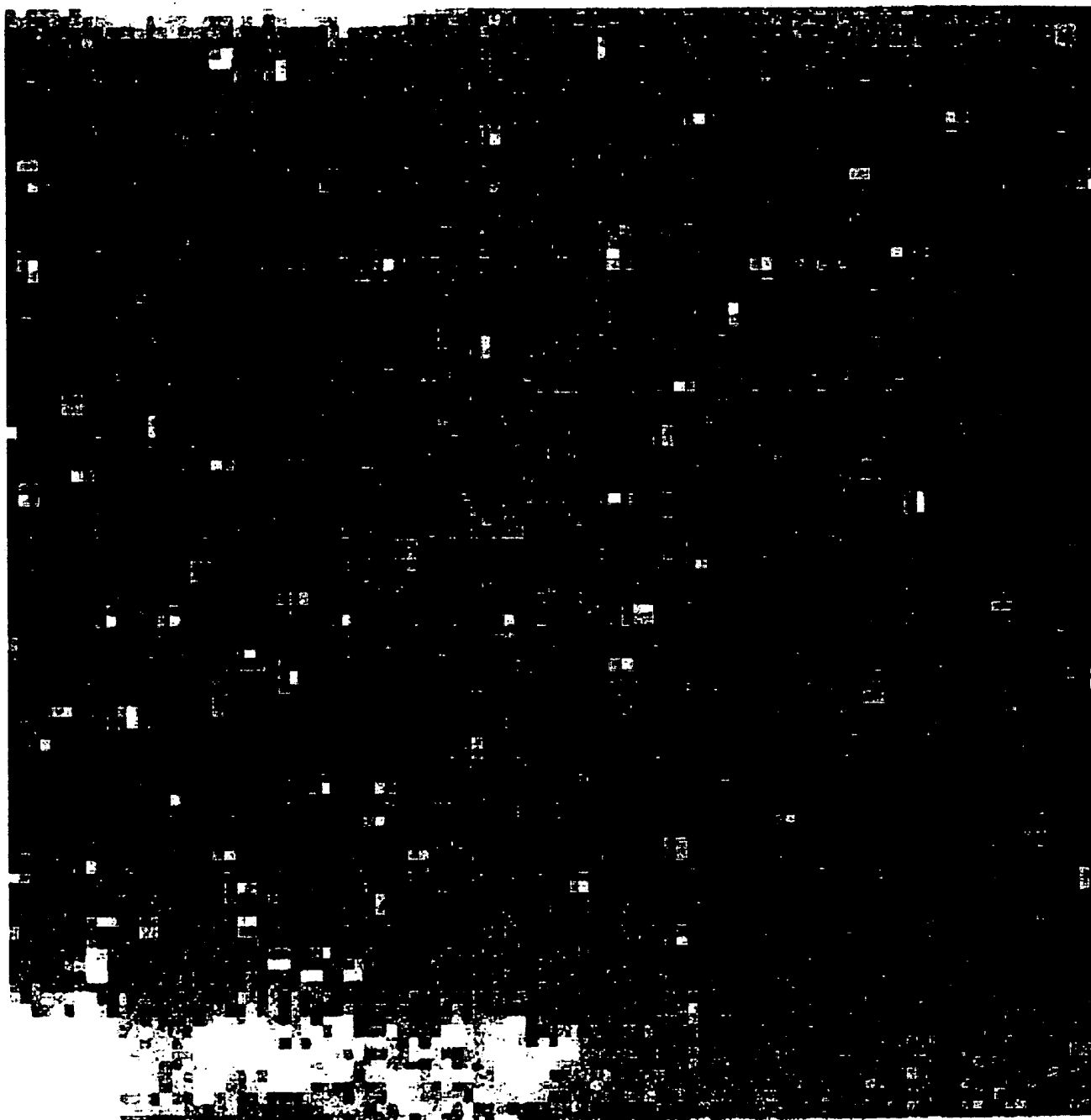


Figure 18



Sulfurylase on mobile support/Luciferase on surface, PPi flows across FORA surface. 1 mobile-support per pixel on camera; 50 μ m FORA well spanning 4 15 μ m pixels. Shown is 100 x 100 Pixels (10K pixels), 1.5 mm².

Figure 19

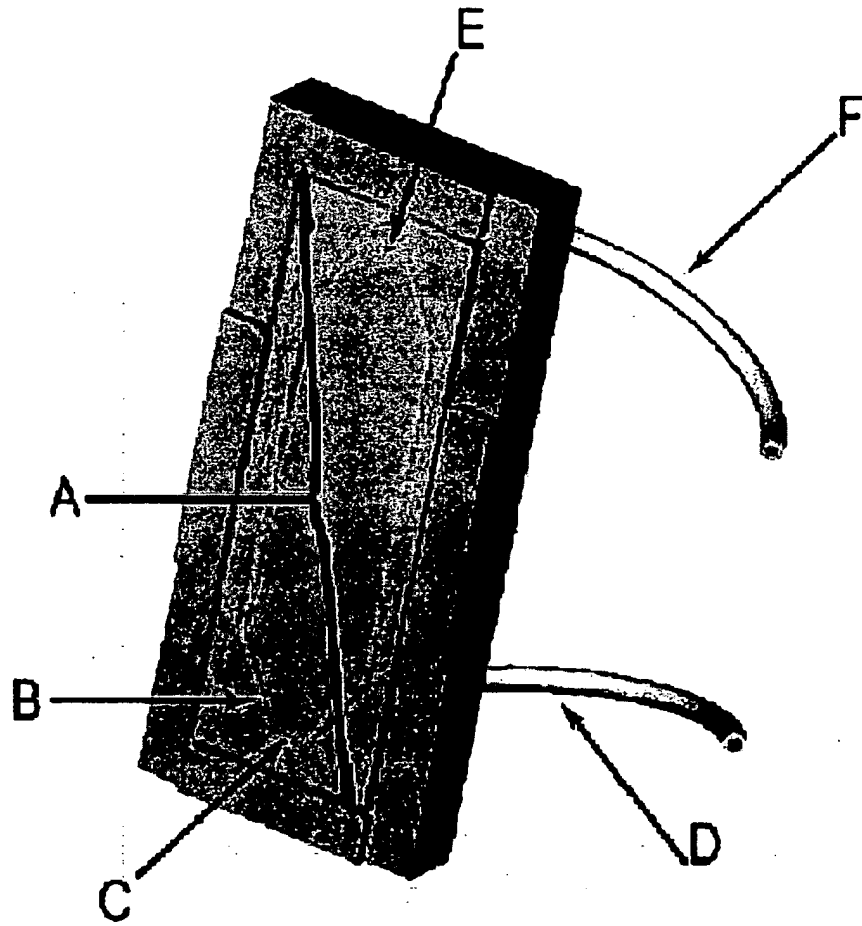


Figure 20

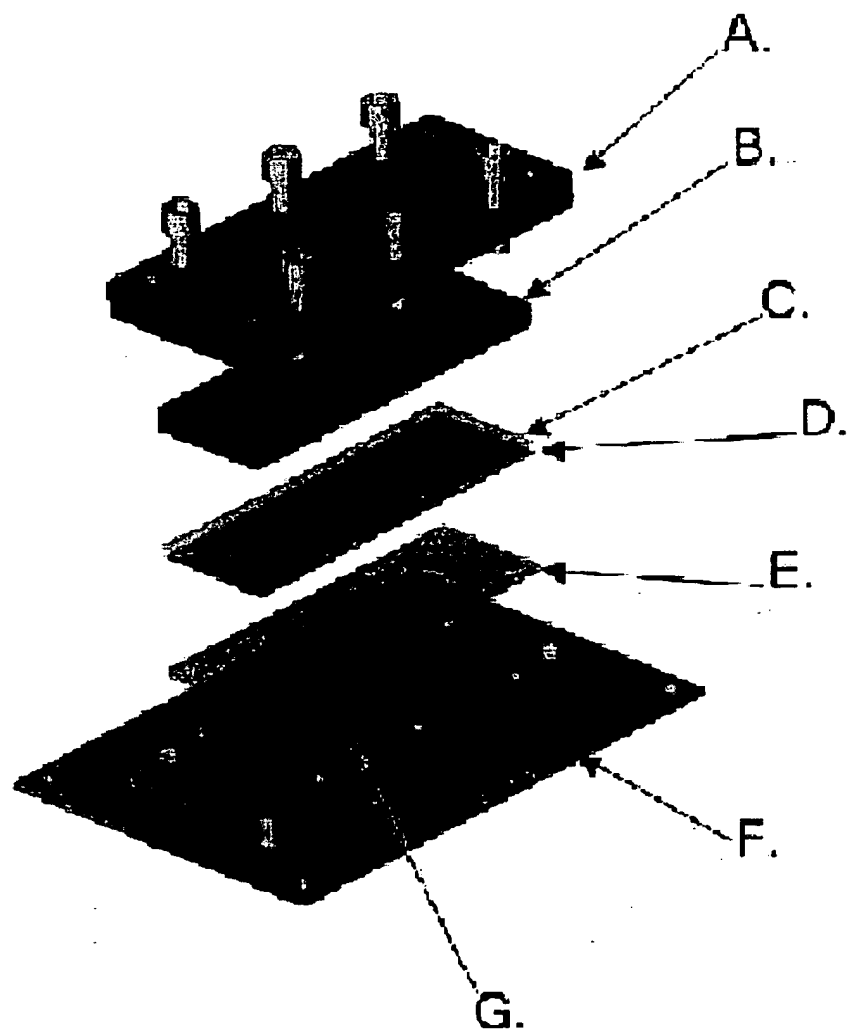


Figure 21

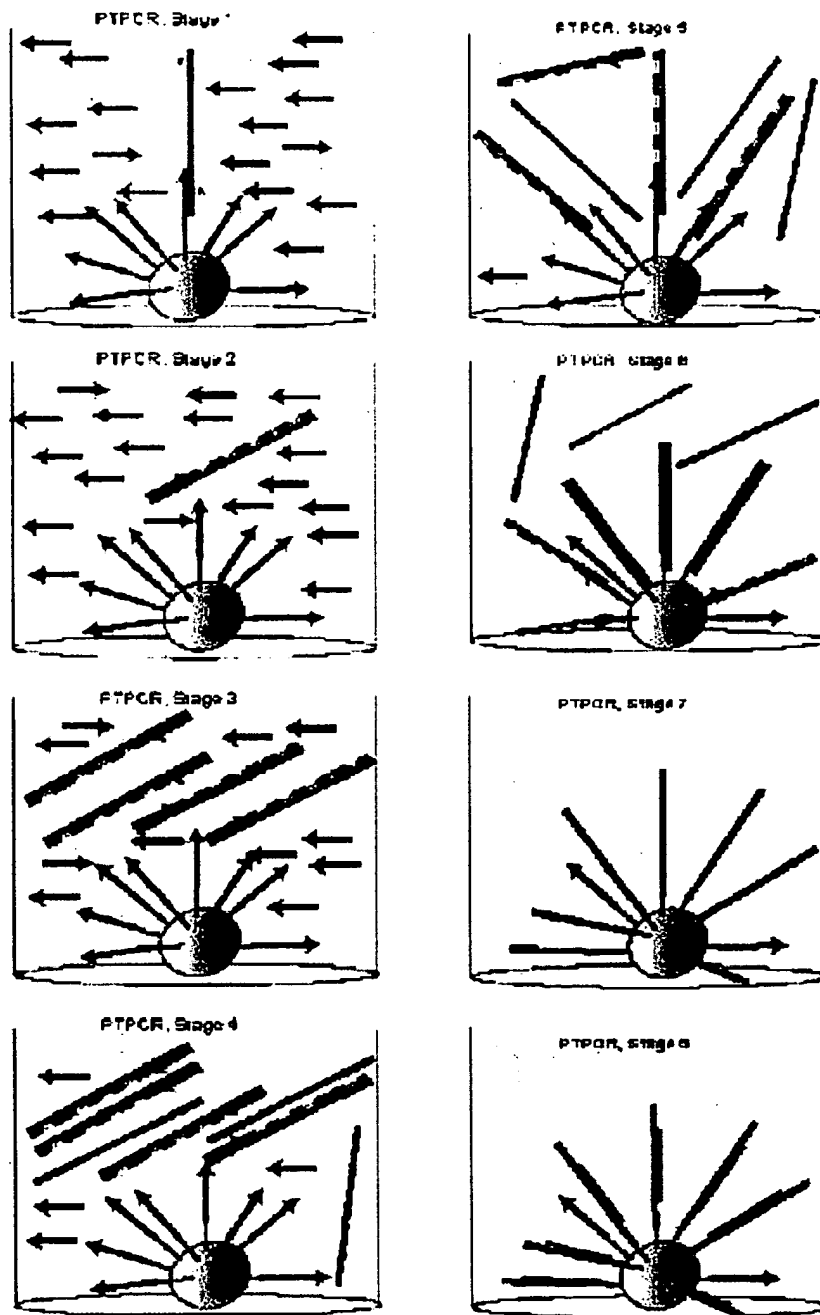


Figure 22

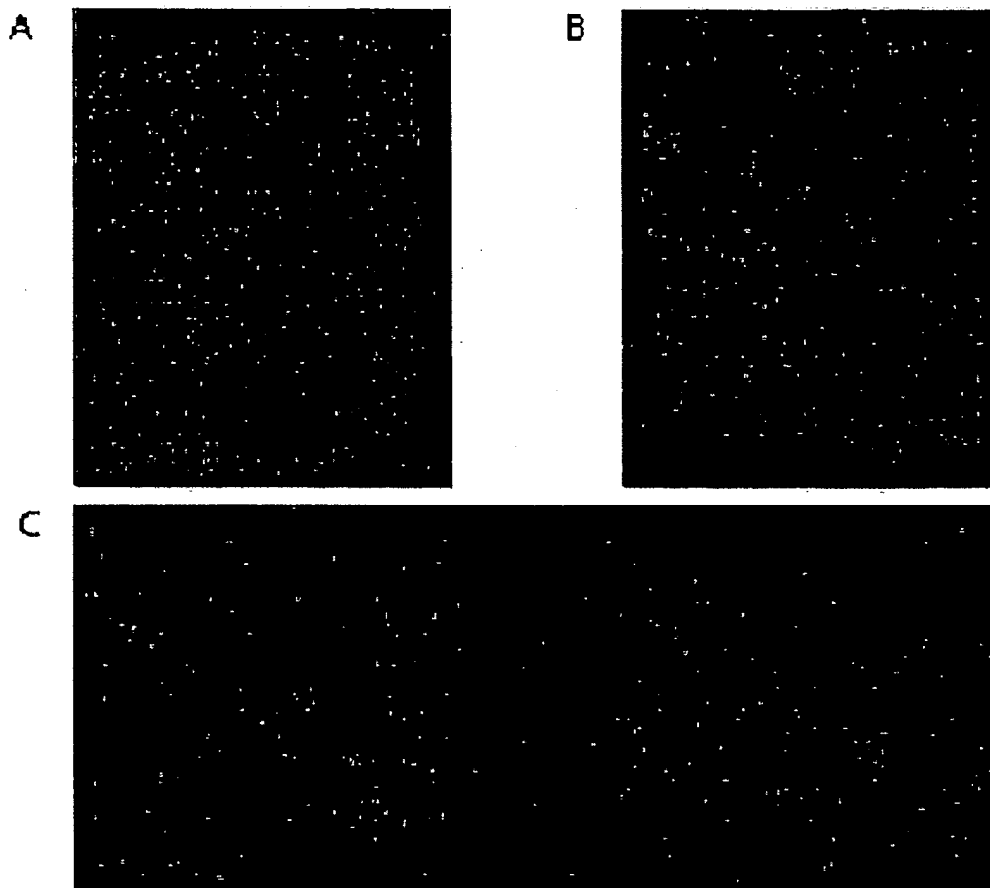


Figure 23

Figure 24

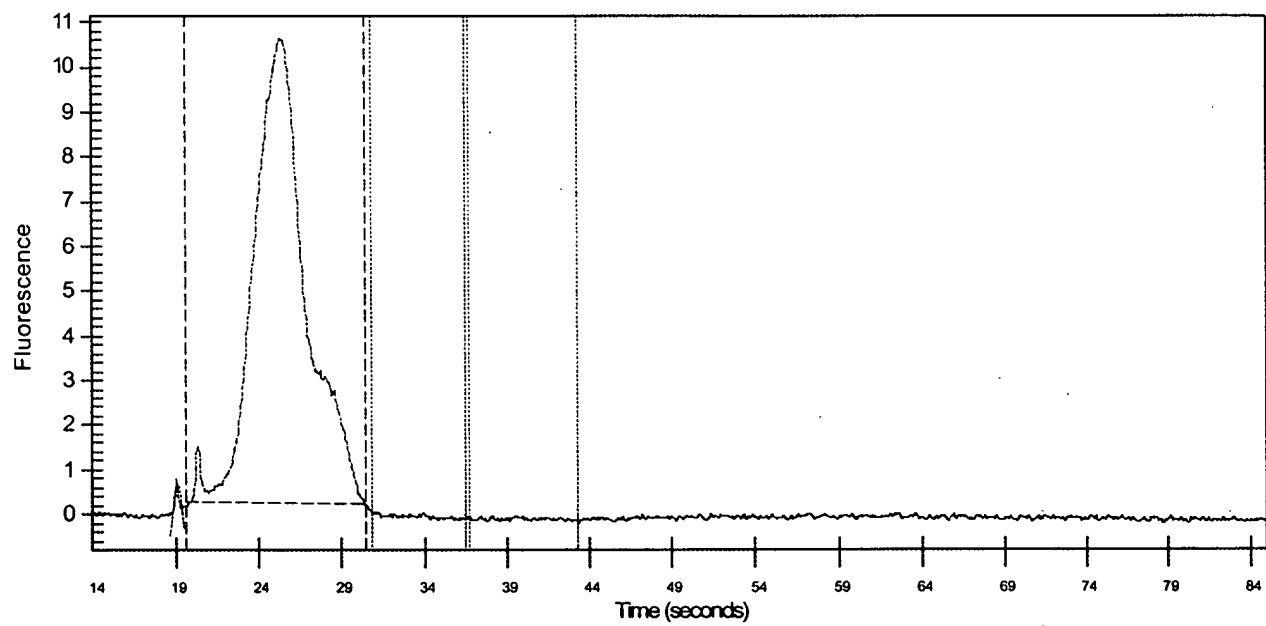


Figure ~~24~~ 25

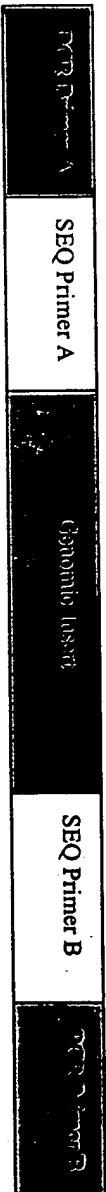


Figure ~~26~~ 26

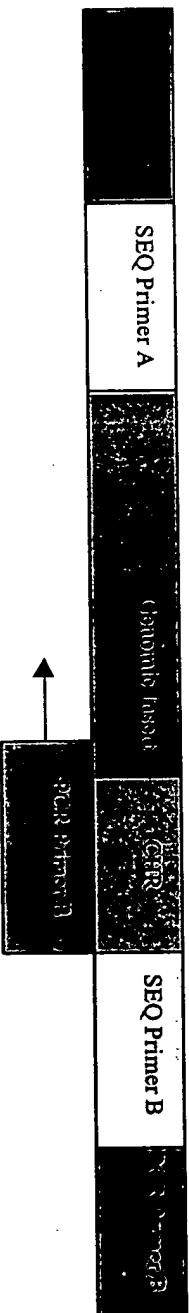


Figure 27

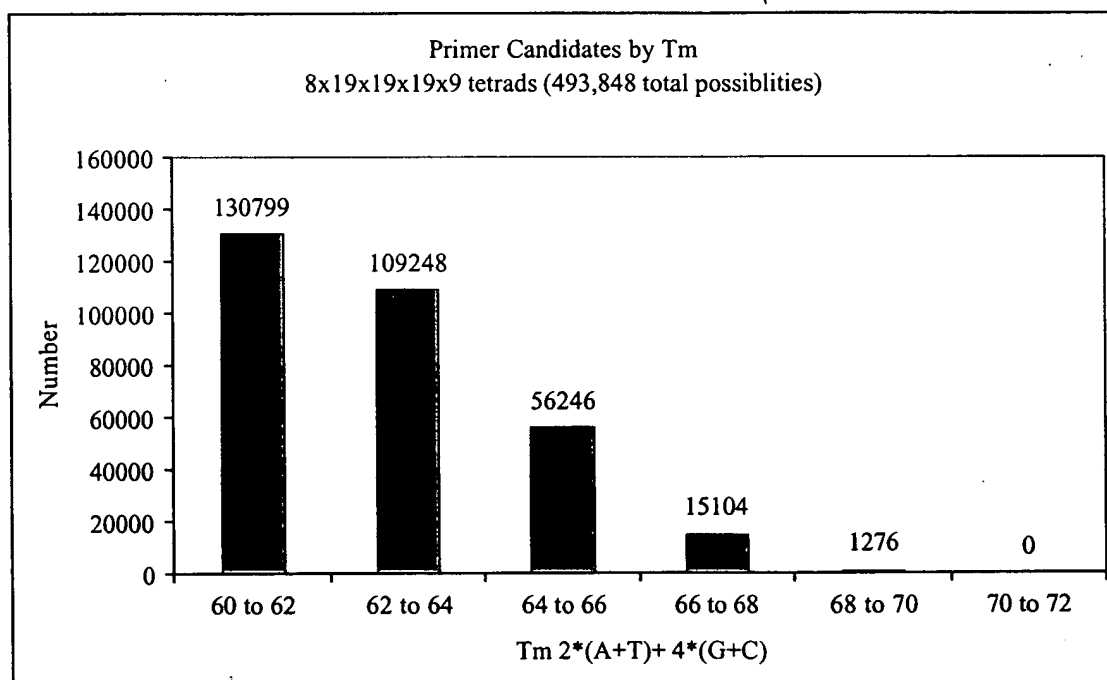


Figure 28

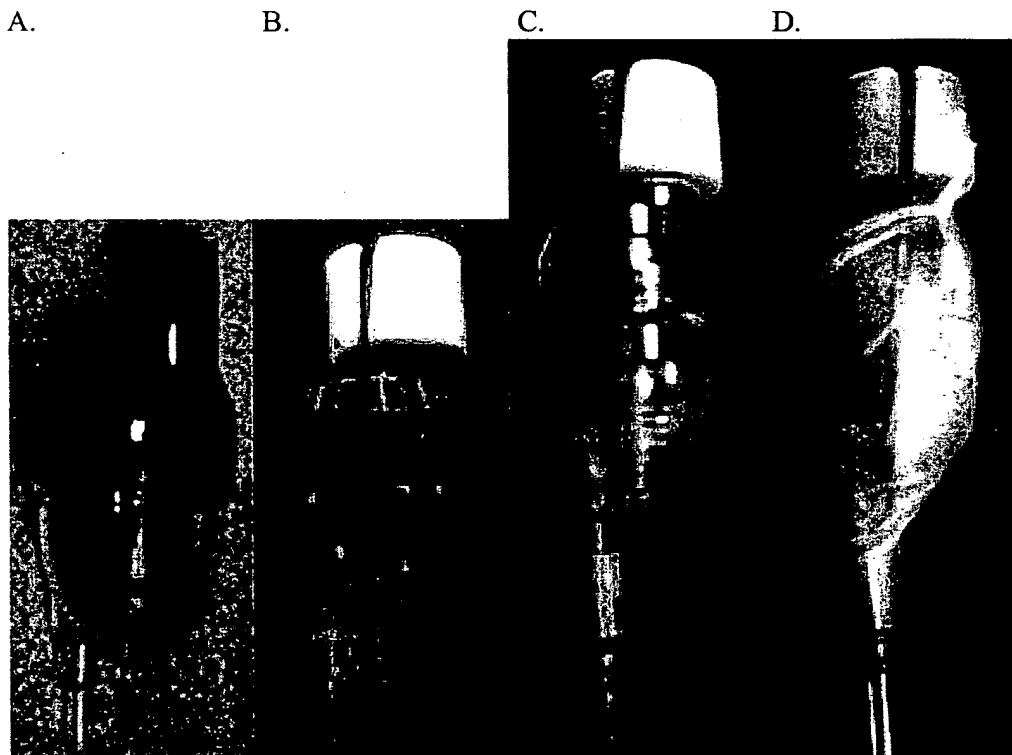


Figure 29A

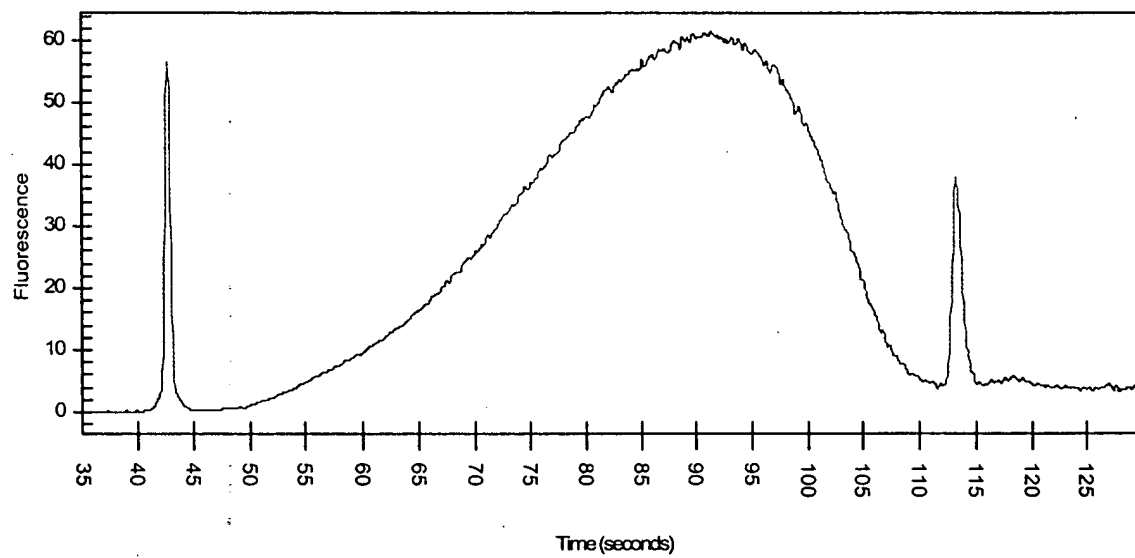


Figure 29B

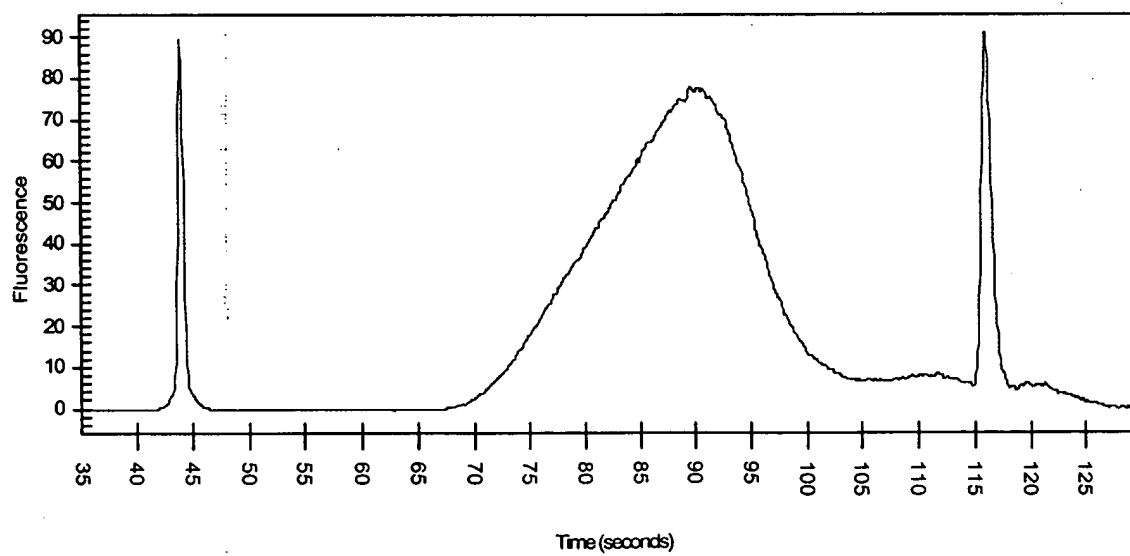




Figure 30

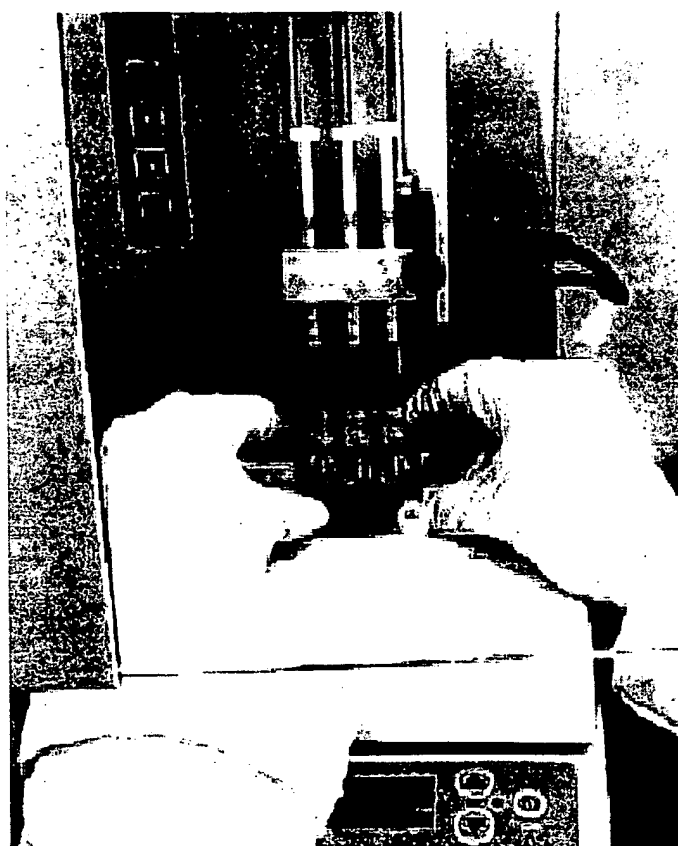


Figure 31

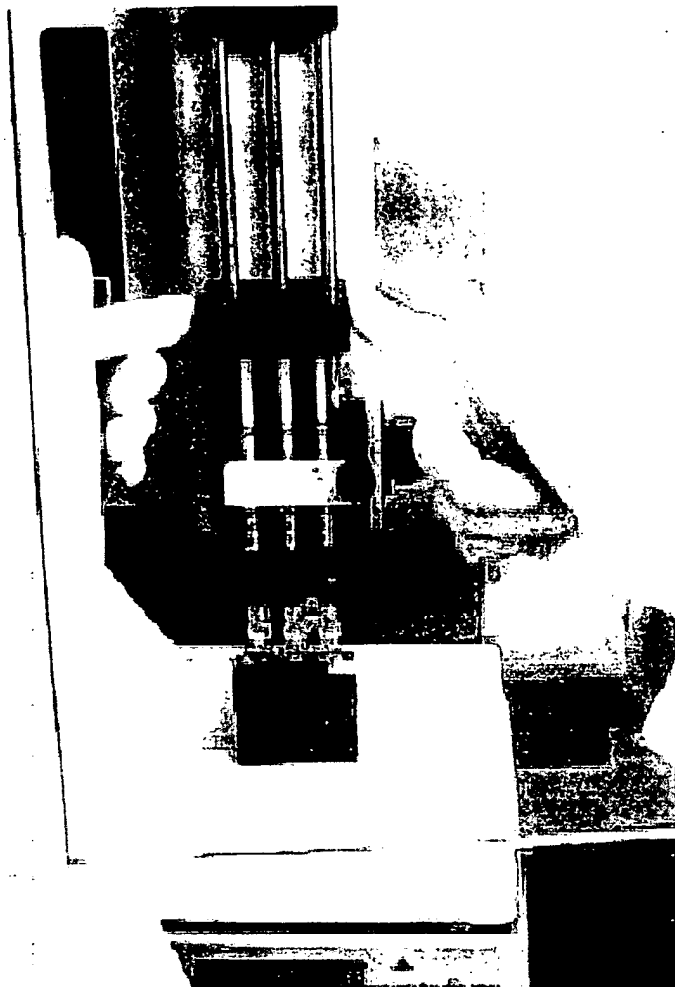


Figure 32

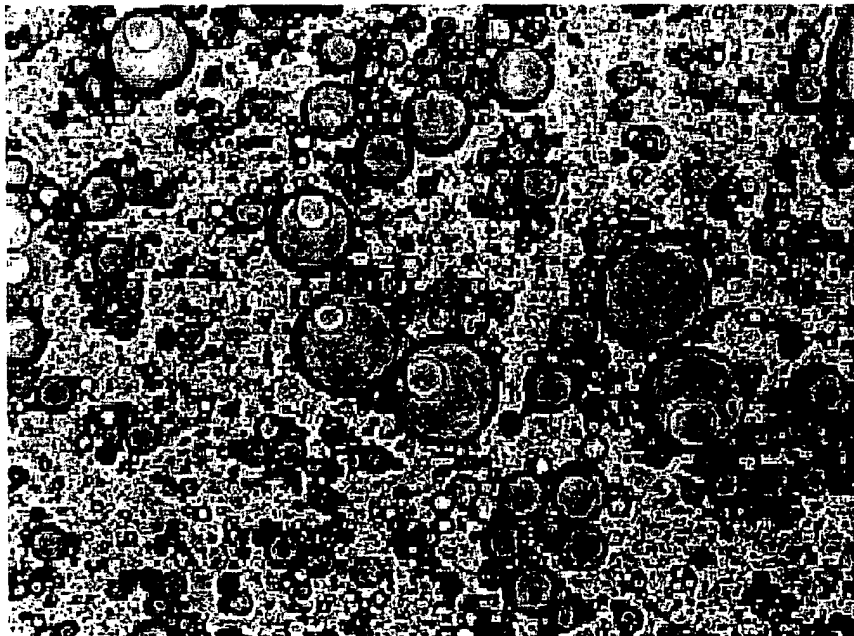
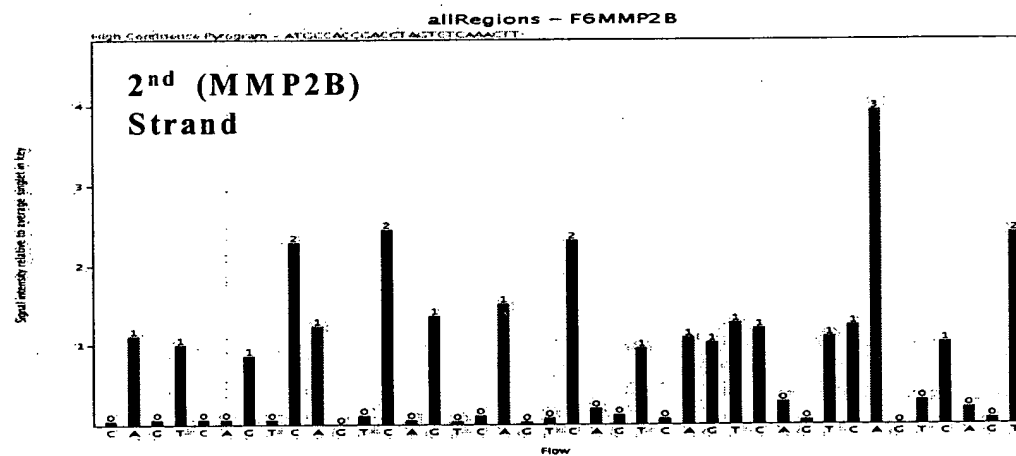
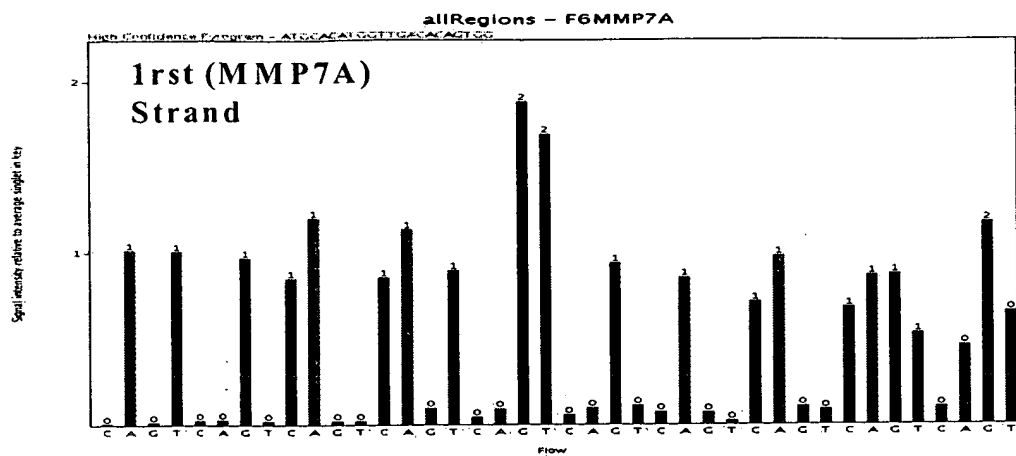


Figure 33

FIGURE 34



1st Strand (MMP7A)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00001_1362_1660.well	ATGCACATGGTTGACACAGTGGT	22

ATGC ACATGGTTGACACAGTGG

2nd Strand (MMP2B)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00003_1363_1660.well	ATGCCACCGACCTAGTCTCAAACCTT	25

ATGC CACCGACCTAGTCTCAAACCTT

Fig. 35

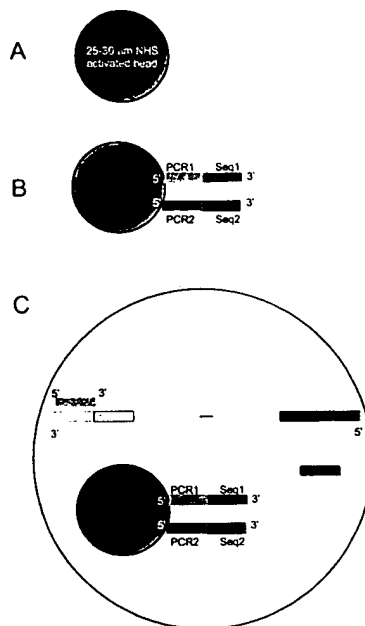


Fig. 36

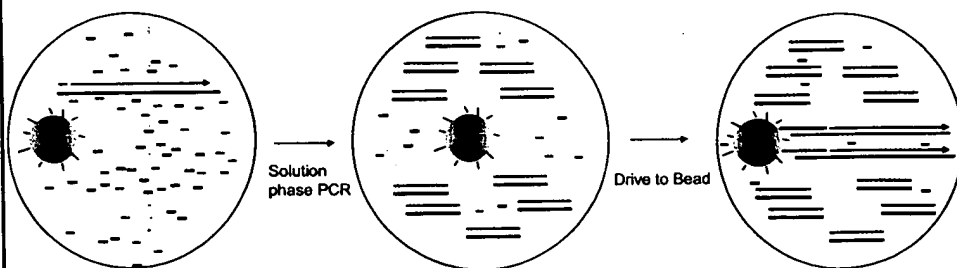


Fig.37

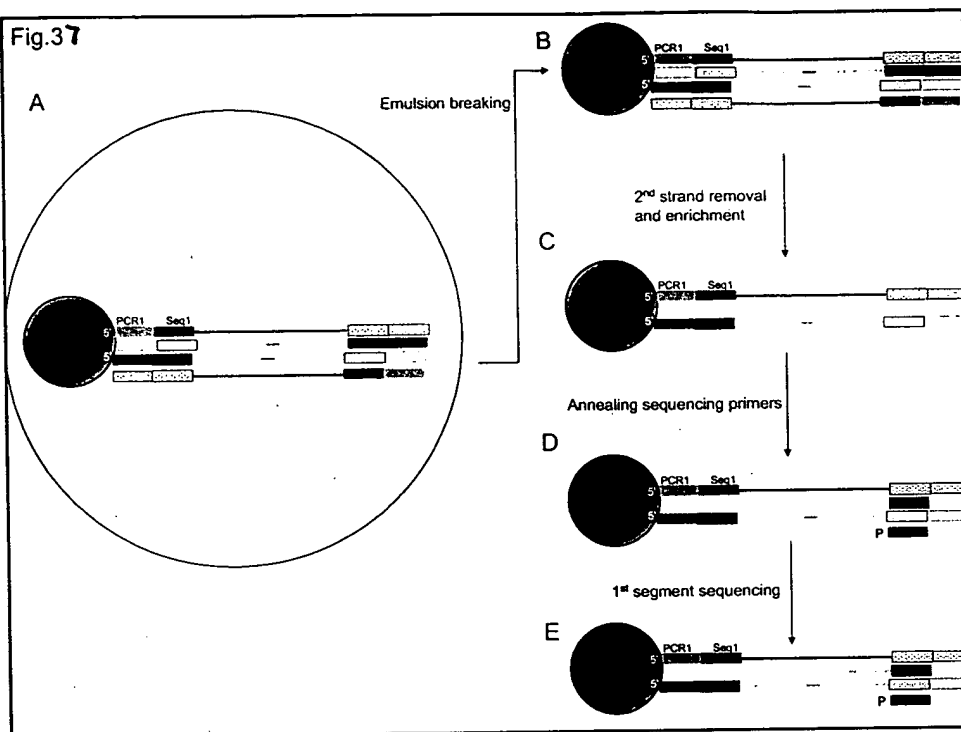


Fig. 38

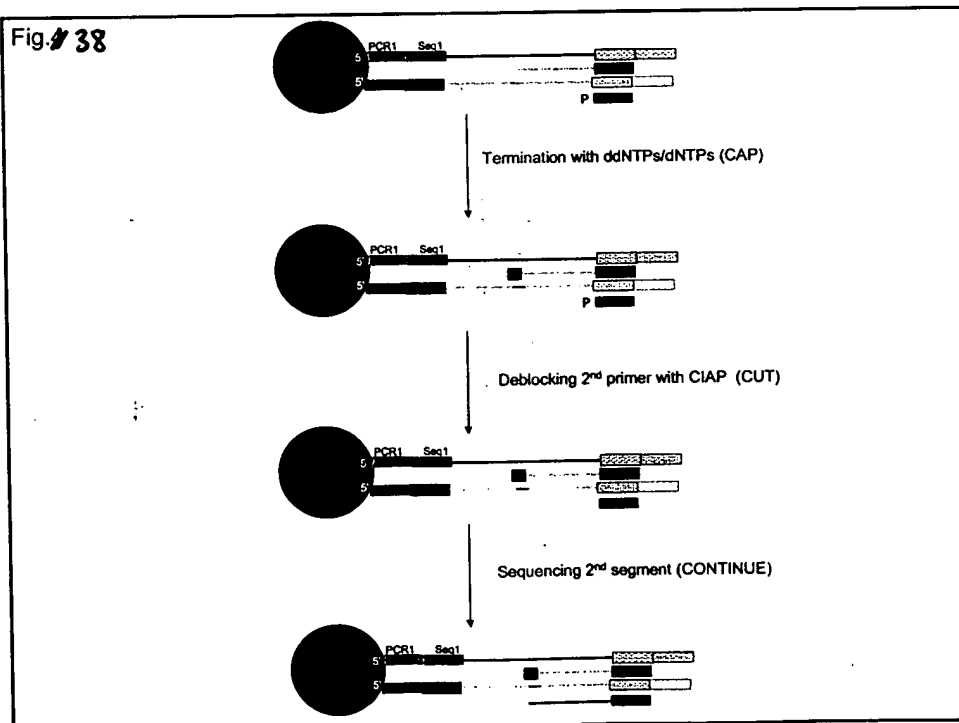
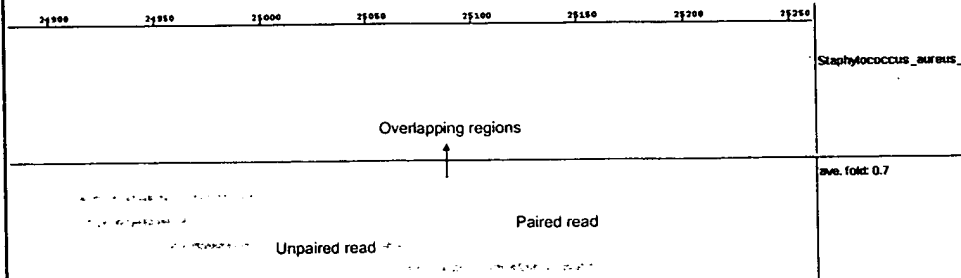


Fig. 39

A



B

Total Reads	31,785
Total 1st Strand	15,770
Total 2nd strand	16,015
Paired	11,799
Non Paired Reads	8,187
Total Coverage	38%

Fig. 40

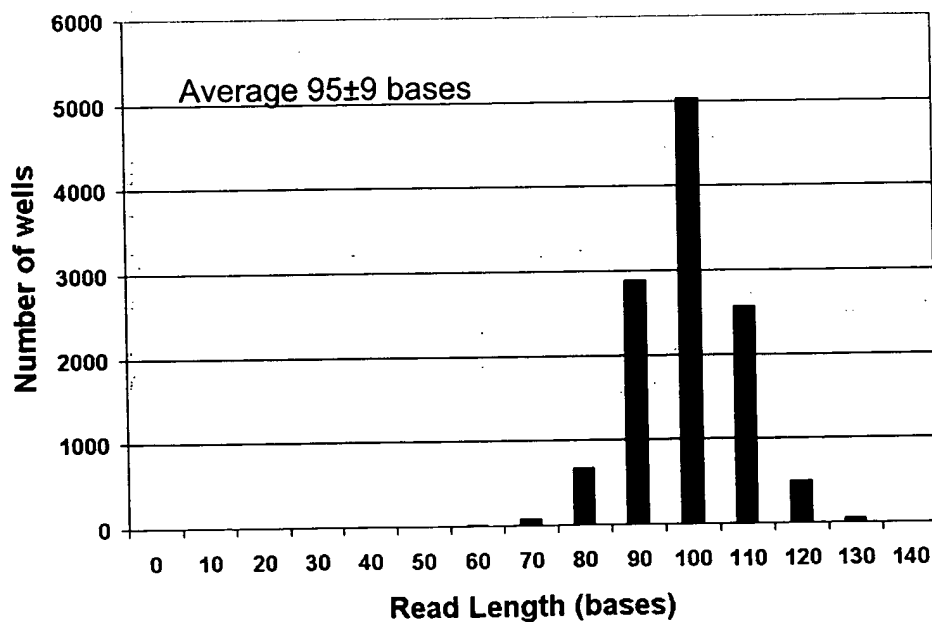


Fig. 41

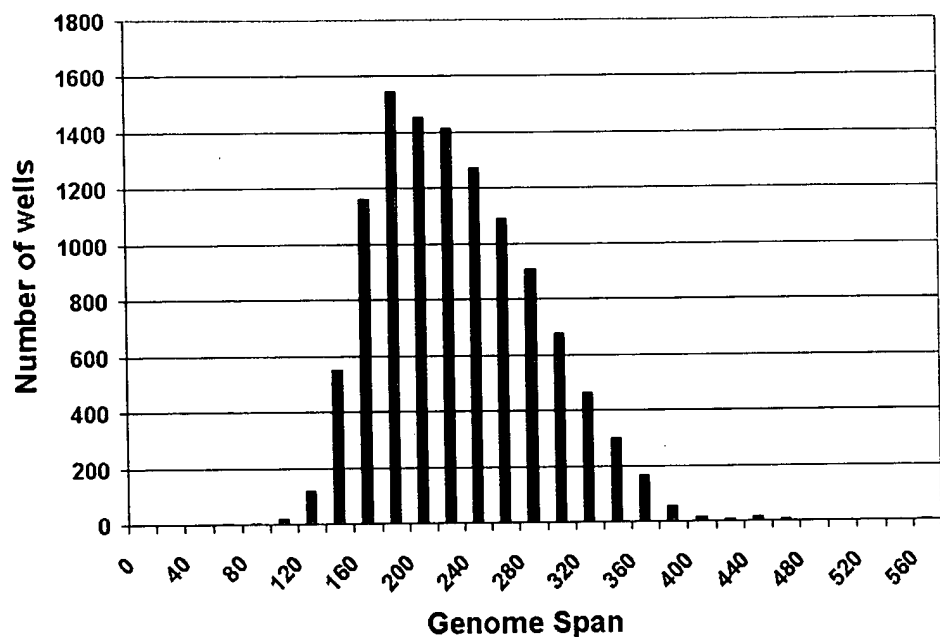


Fig. 42

Well	Genome Position	Orientation	Alignment String
00364 0548 2509	571366	F	TATTGTTGATGCTGTAAAAaGAAGCTACTGGTGTAGIATTTTATGAAGTT
00364 0548 2509 D2	571512	R	TGCTCAAAGAATTCATTAAAAATGACCATAITTCATTGTATCTTT
00363 0985 2232	1487890	R	AAGCGAACAGTCAAGTACCACAGTCAGTTGACITTTACACAAGCGGAT
00363 0985 2232 D2	1487769	F	TACAGGTGTTGGTATGCCATTGCGATTGTTGCGCTTGGTTAGCCG
00397 0940 2923	2611033	F	AACATATAAACATCCCCTATCTCAATTCGCTTCCATGTAaCAAAAAAGC
00397 0940 2923 D2	2611164	R	TAGATATCACTTGCCTGTACTGGTAATGCAGGCATGAG
00417 0611 1933	122001	R	ATTCAACTCTGGAATGCITTCCTGATACGCCCTCGATGATG
00417 0611 1933 D2	121930	F	GATGAGGAGCTGCAATGGCAATGGGTAAAGGCATCATCG
00434 0595 0993	2022591	R	TGTATCTCGATTGGATTAGTTGCTTTTGCATCTTCATTAGACC
00434 0595 0993 D2	2022473	F	CATTAACATCTGCACCAGAAATAGCTTCTAATACGATTGC
00443 1003 0754	107373	F	GCGACGACGTCCAGCTAATAACGCTGCACCTAAGGCTAATGATAAT
00443 1003 0754 D2	107502	R	AAACCATGCAGATGCTAACAAAGCTCAAGCAITACCAGAAACT
00454 1257 3047	59038	R	TGTTGCTGCATCATAATTTAATACTACATCATTTAAITCTTTGG
00454 1257 3047 D2	58880	F	GCAGATGGTGTGACTAACCAAGTTGGTCAAAATGCCCTAAATACAAAAGAT

Figure 15

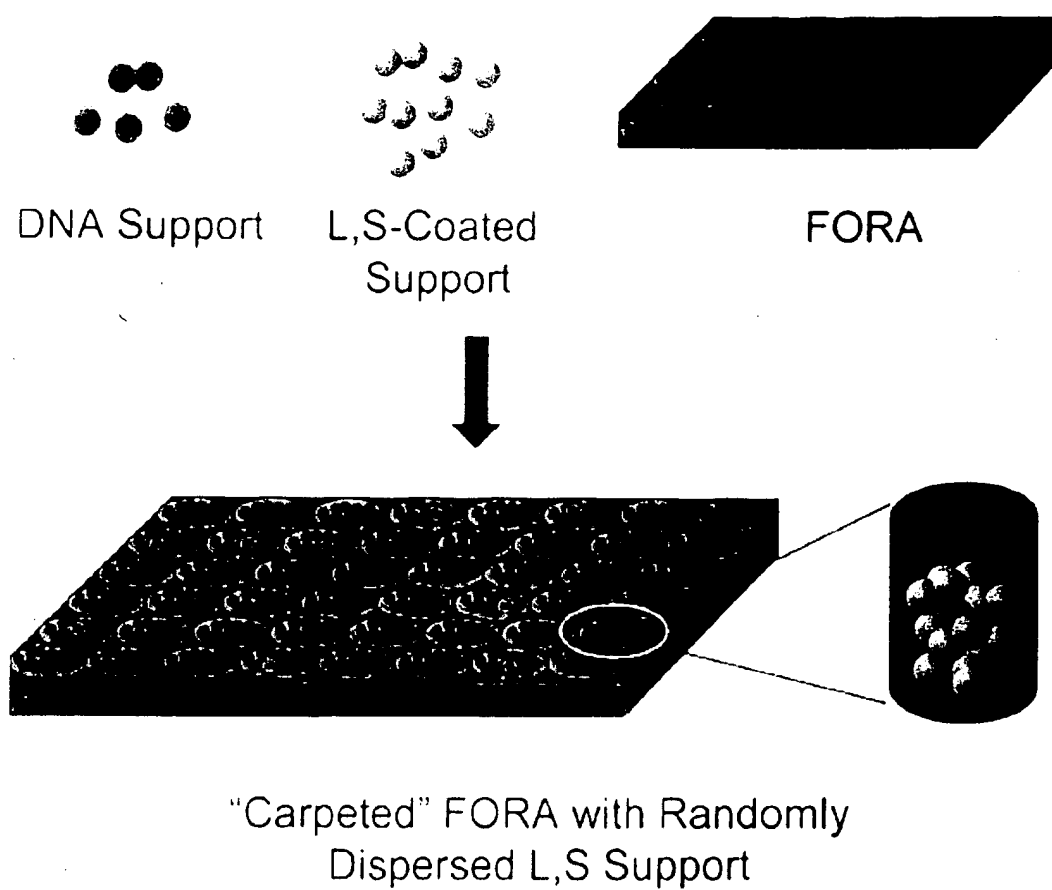


Figure 14

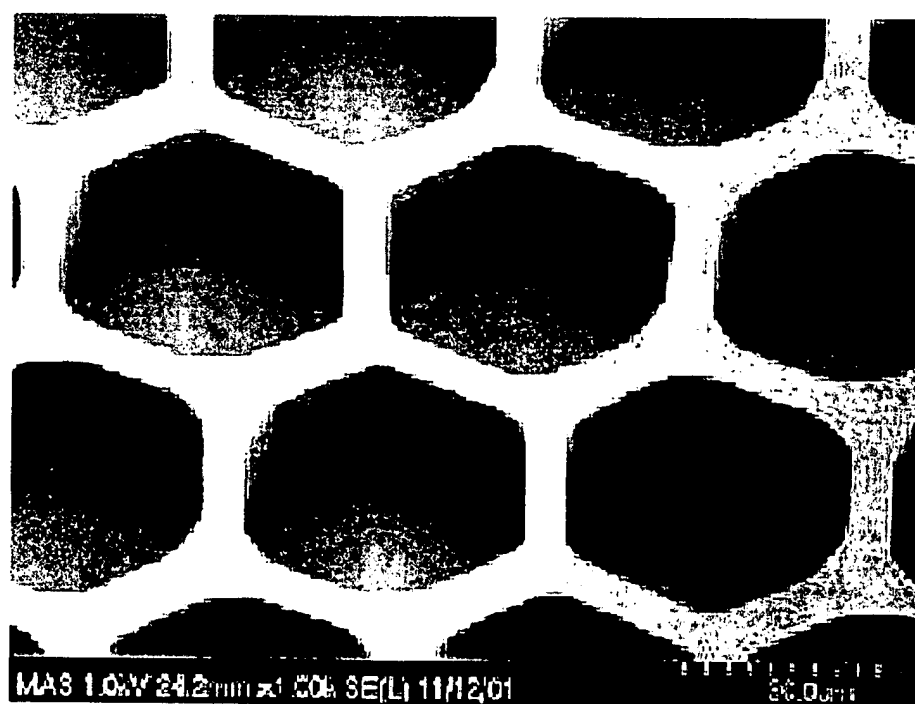
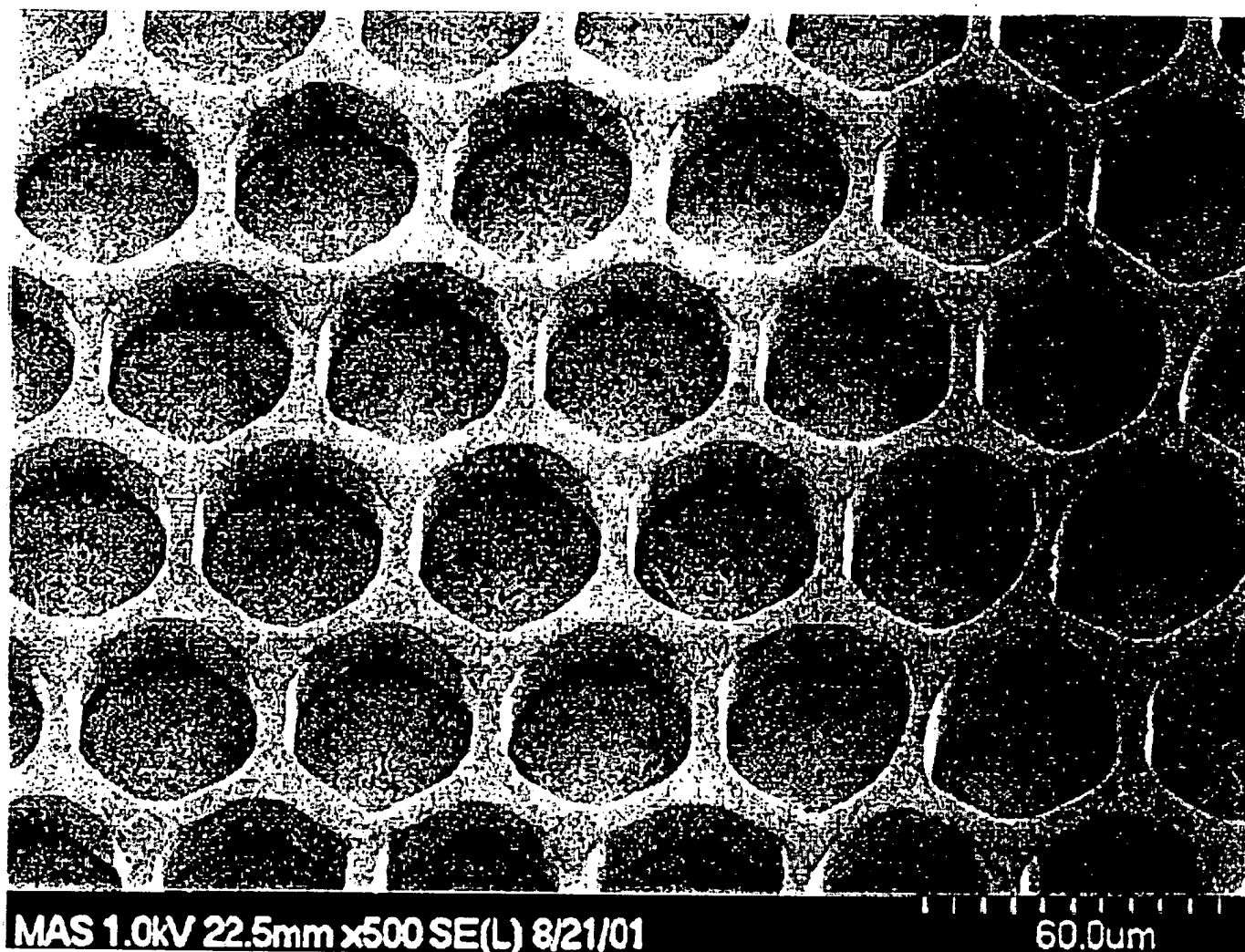


Figure 13

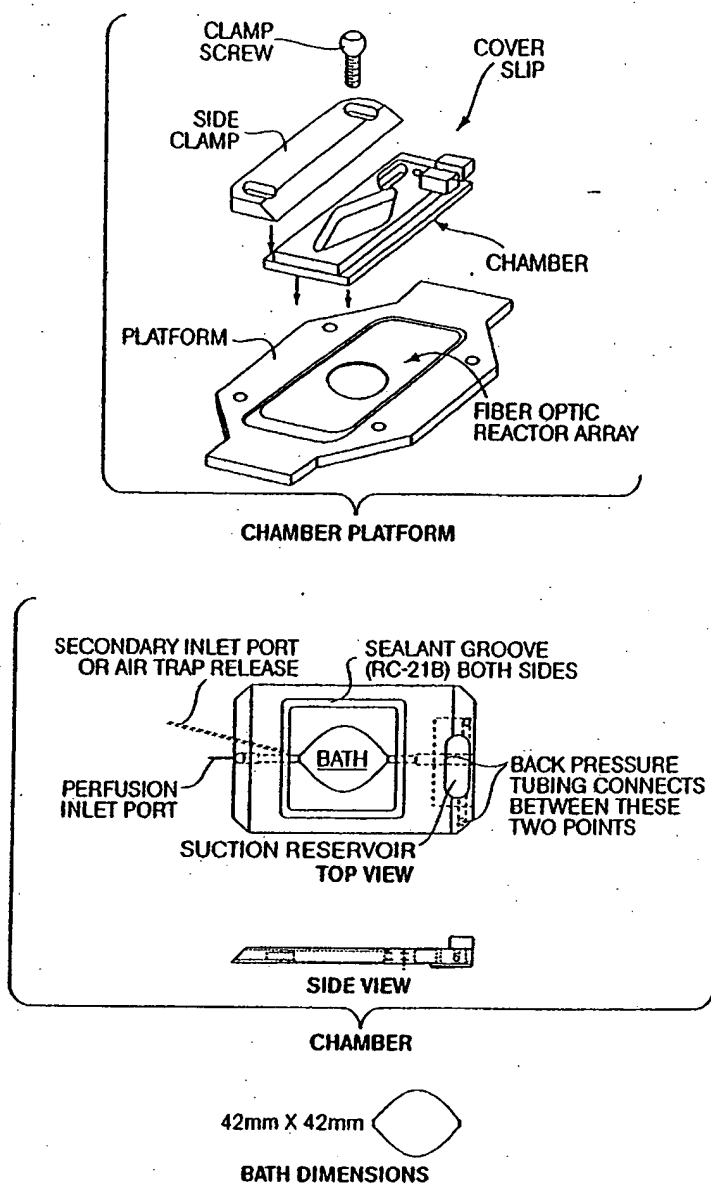


Fig. 3

Figure 12

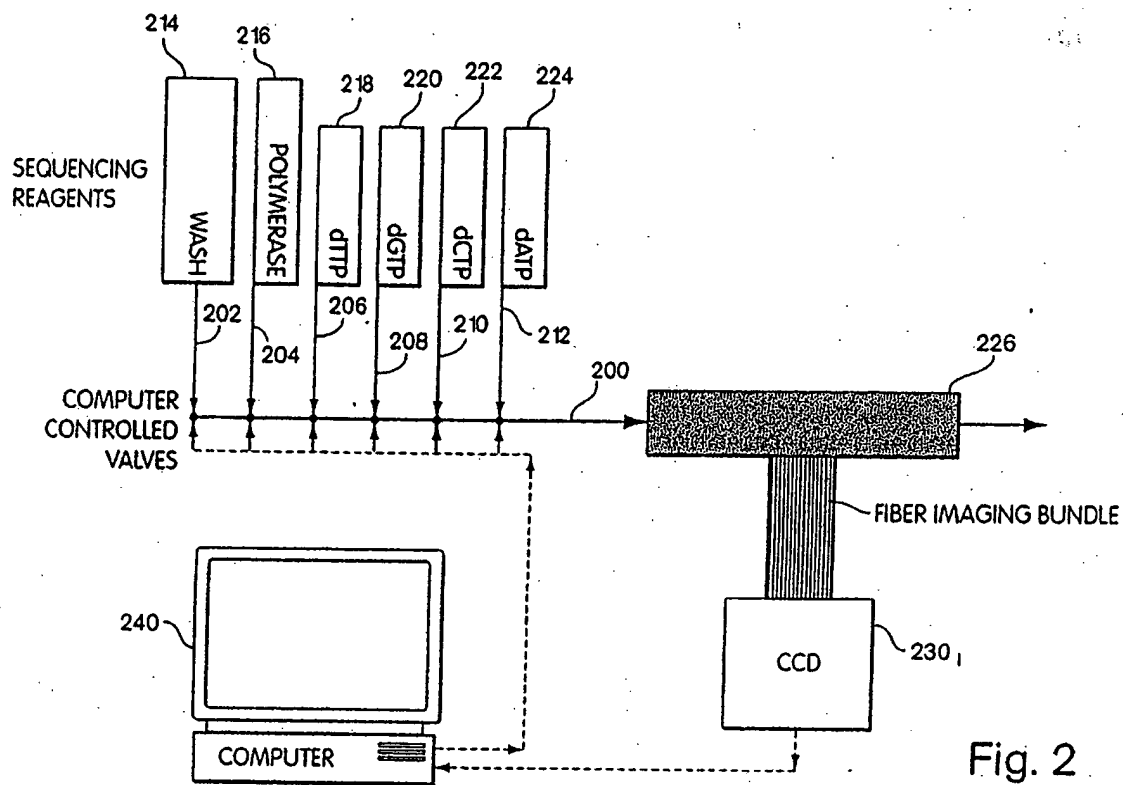


Fig. 2

Figure 11A

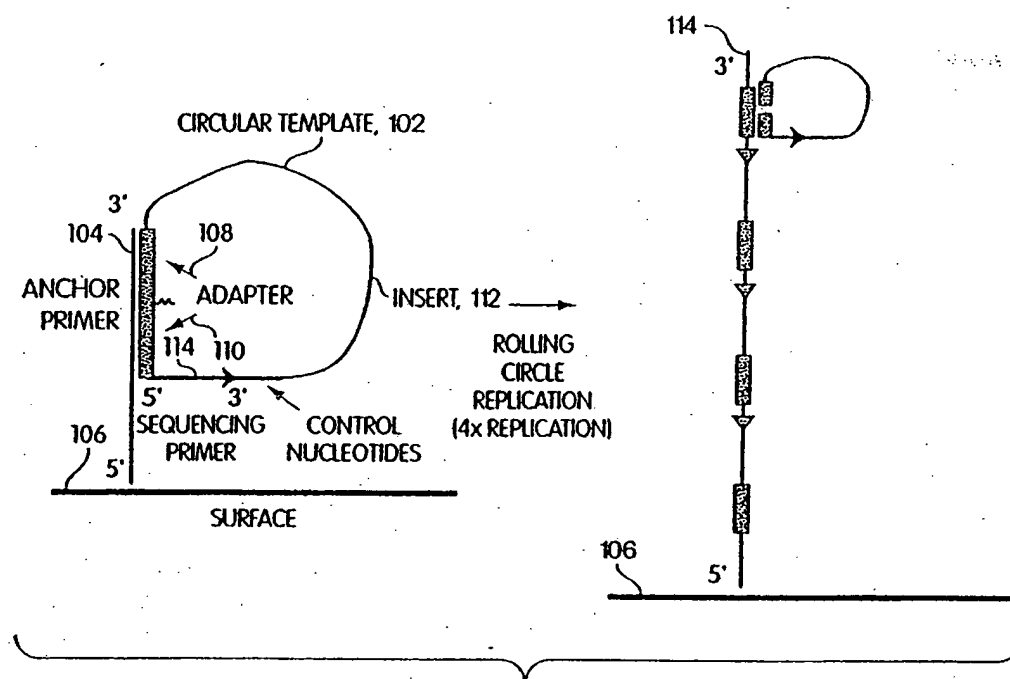


Figure 11B

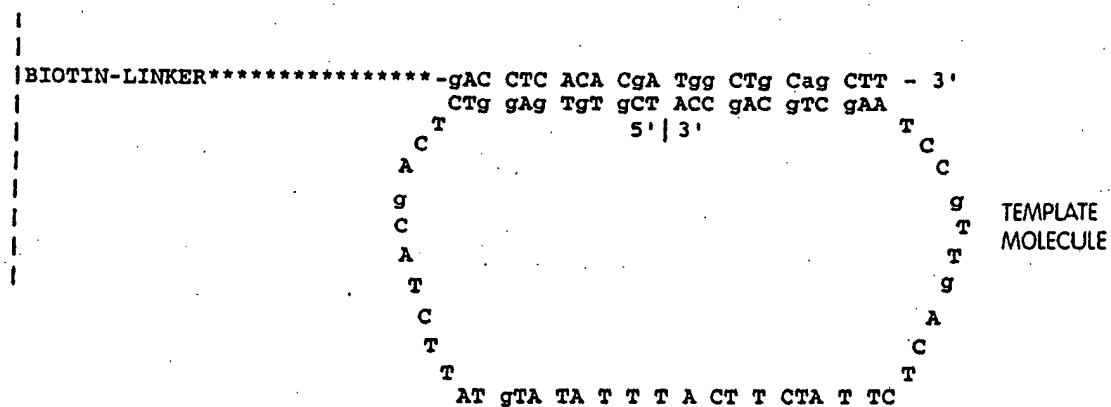
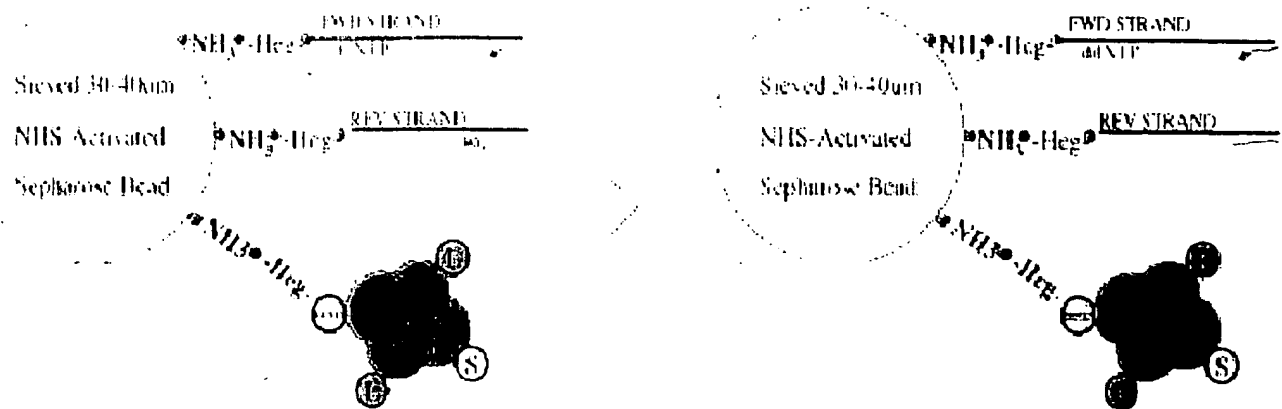
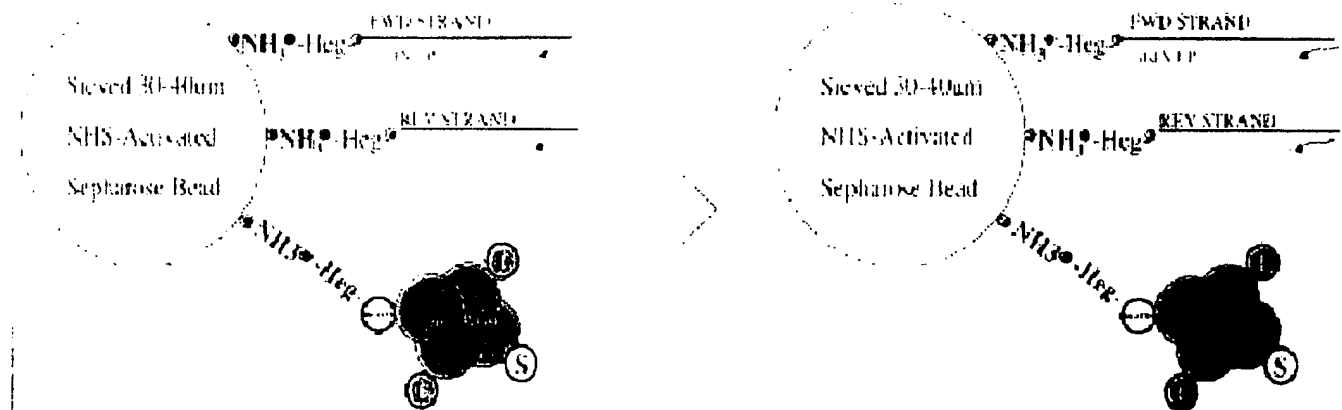


Fig. 1B

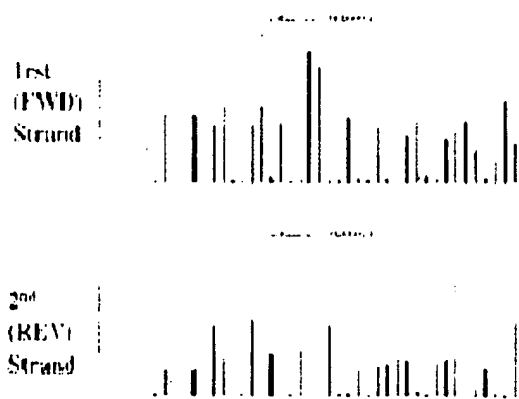
D.)



E.)



F.)

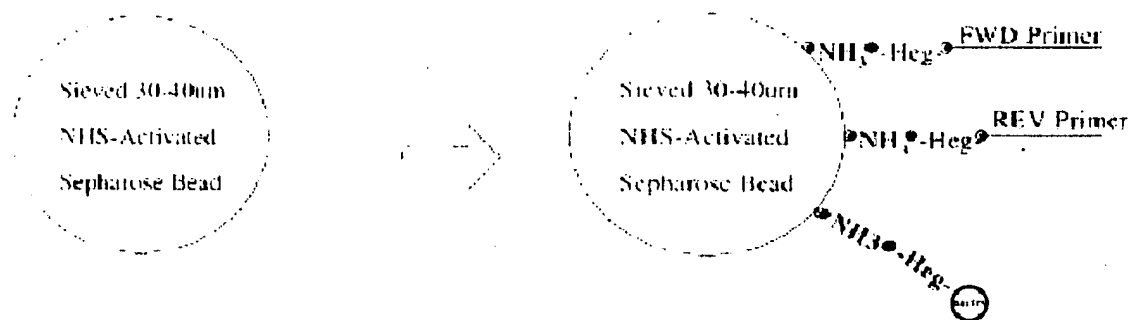


Sample	Read Location	Sequence	Partial Match Length
PG 14.1	10000	5'...TCTT	2

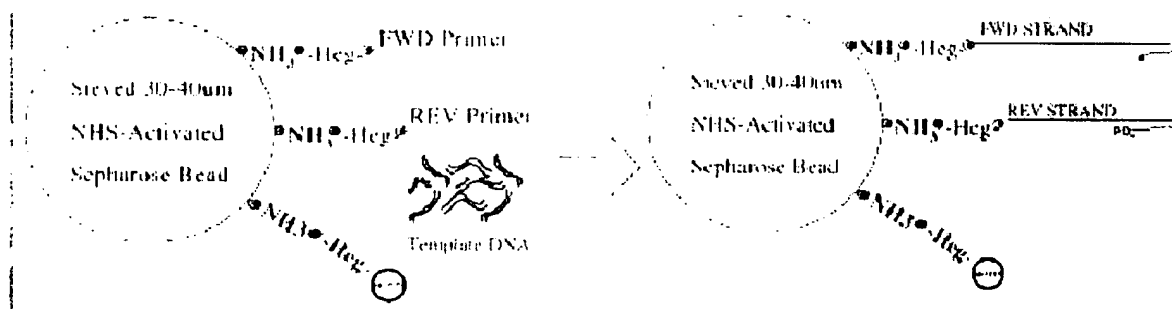
Sample	Read Location	Sequence	Partial Match Length
PG 14.1	10000	3'...AG	2

FIGURE 10

A.)



B.)



C.)

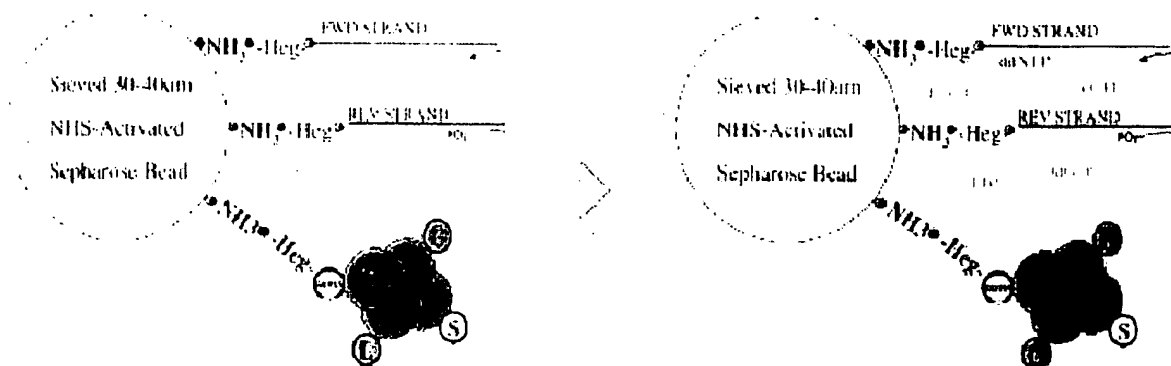
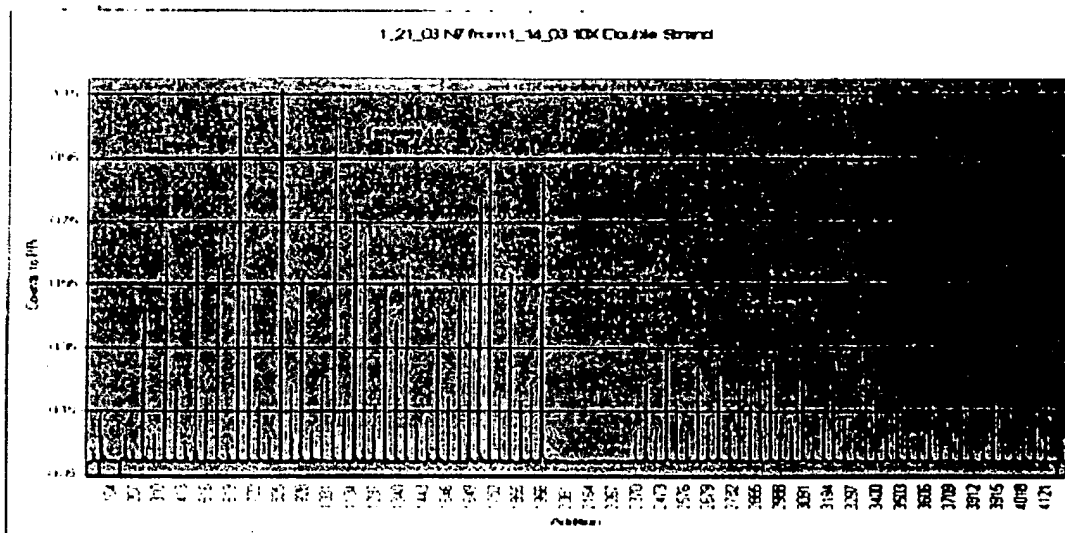


FIGURE 9



NYC 261535v2

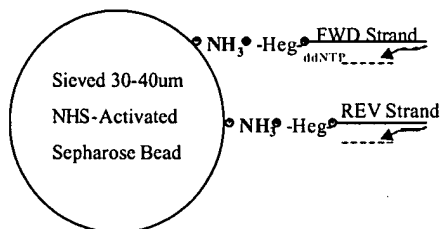
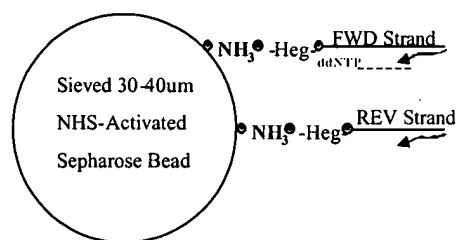
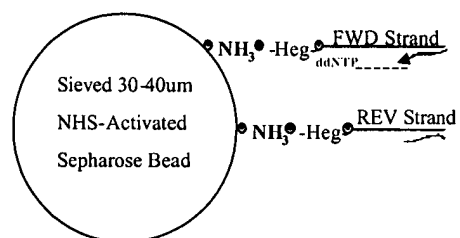
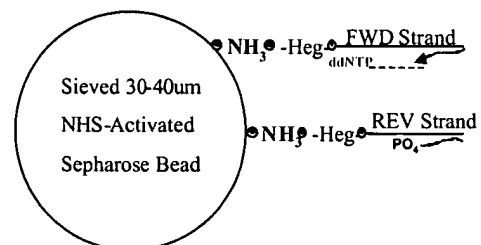
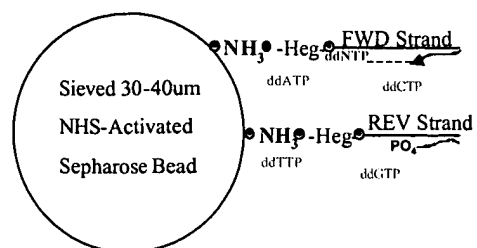


FIGURE 8

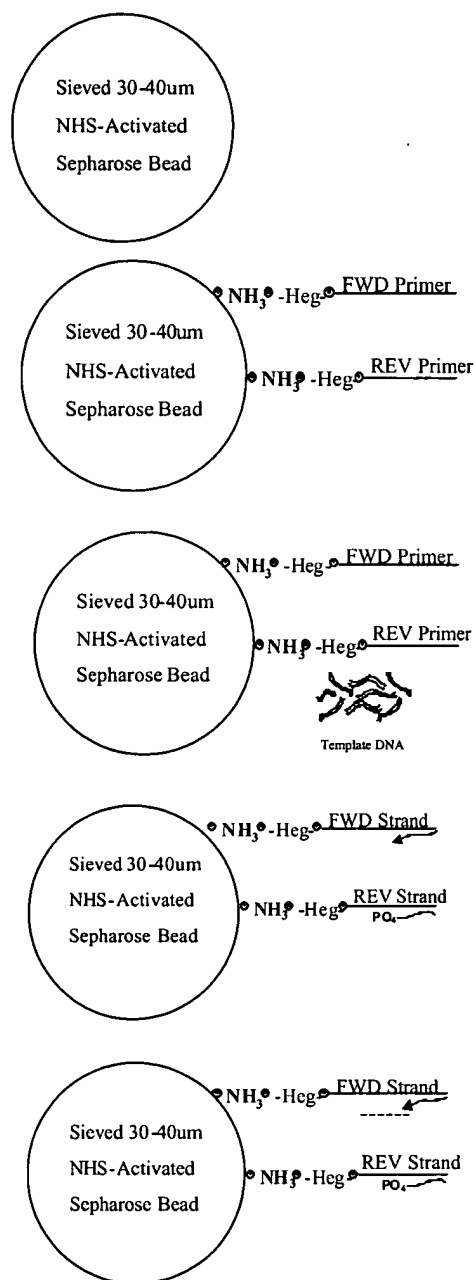


FIGURE 7

Schematic Process Flow for Bead Separation

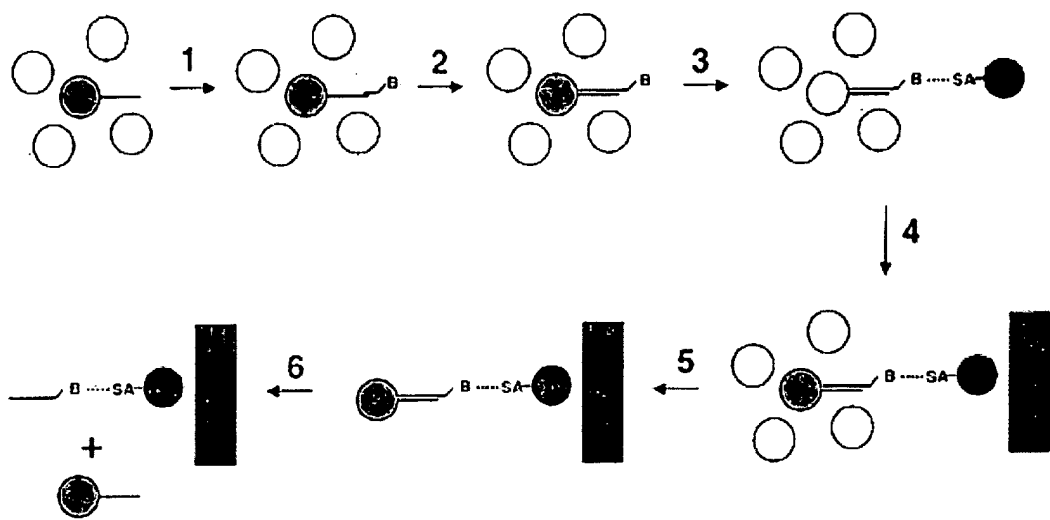


FIGURE 6B

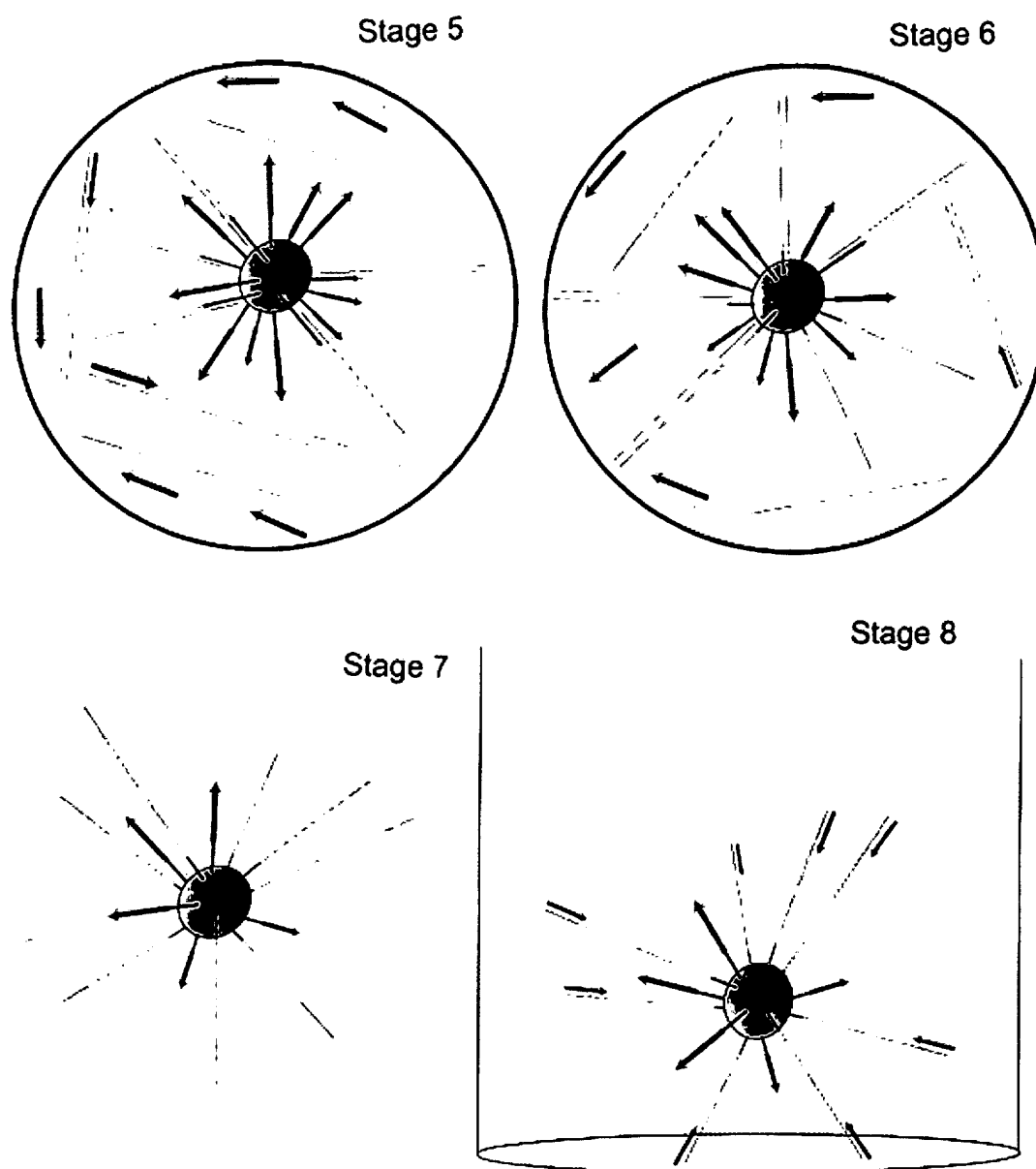


FIGURE 6A

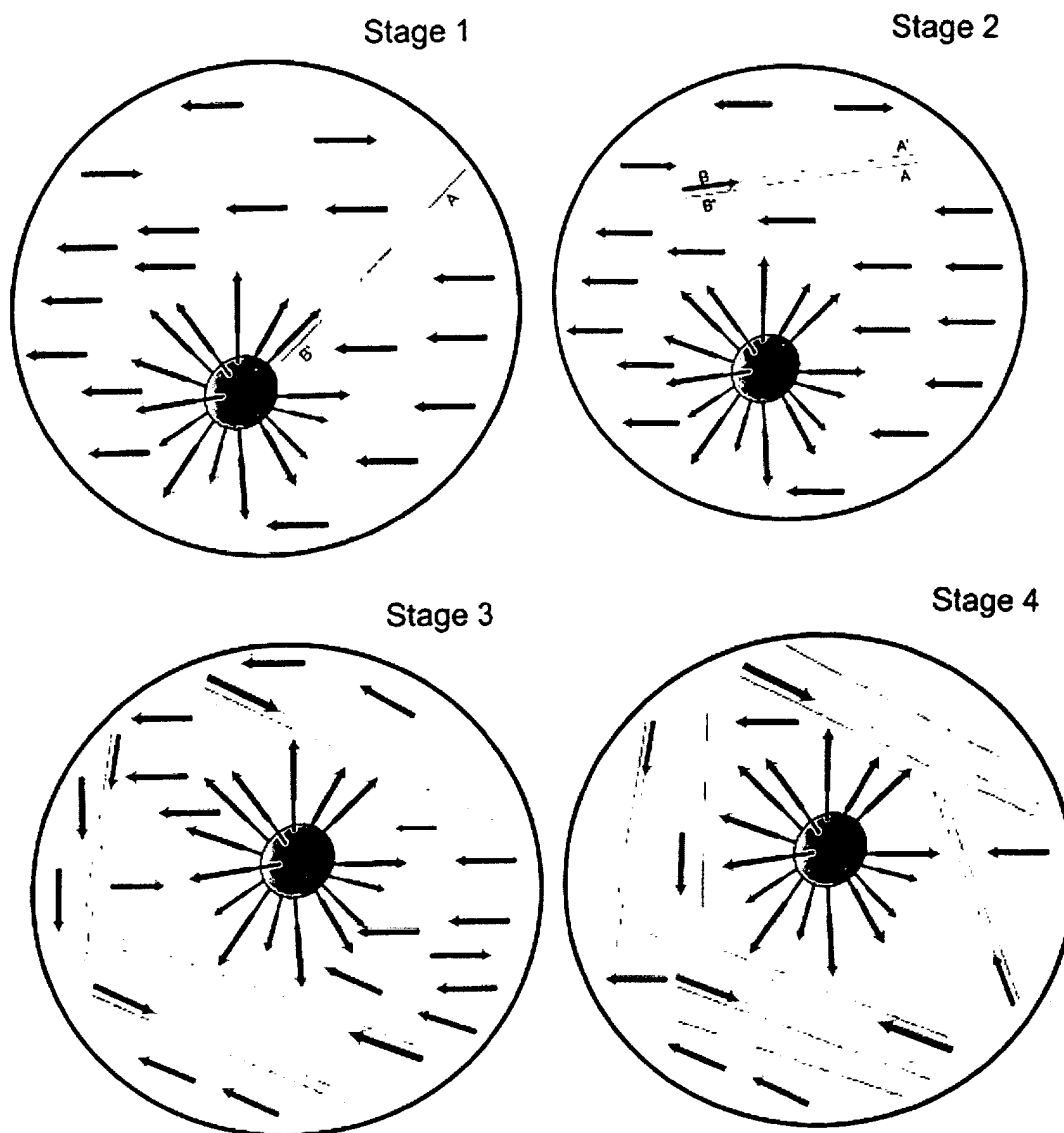


Figure 5

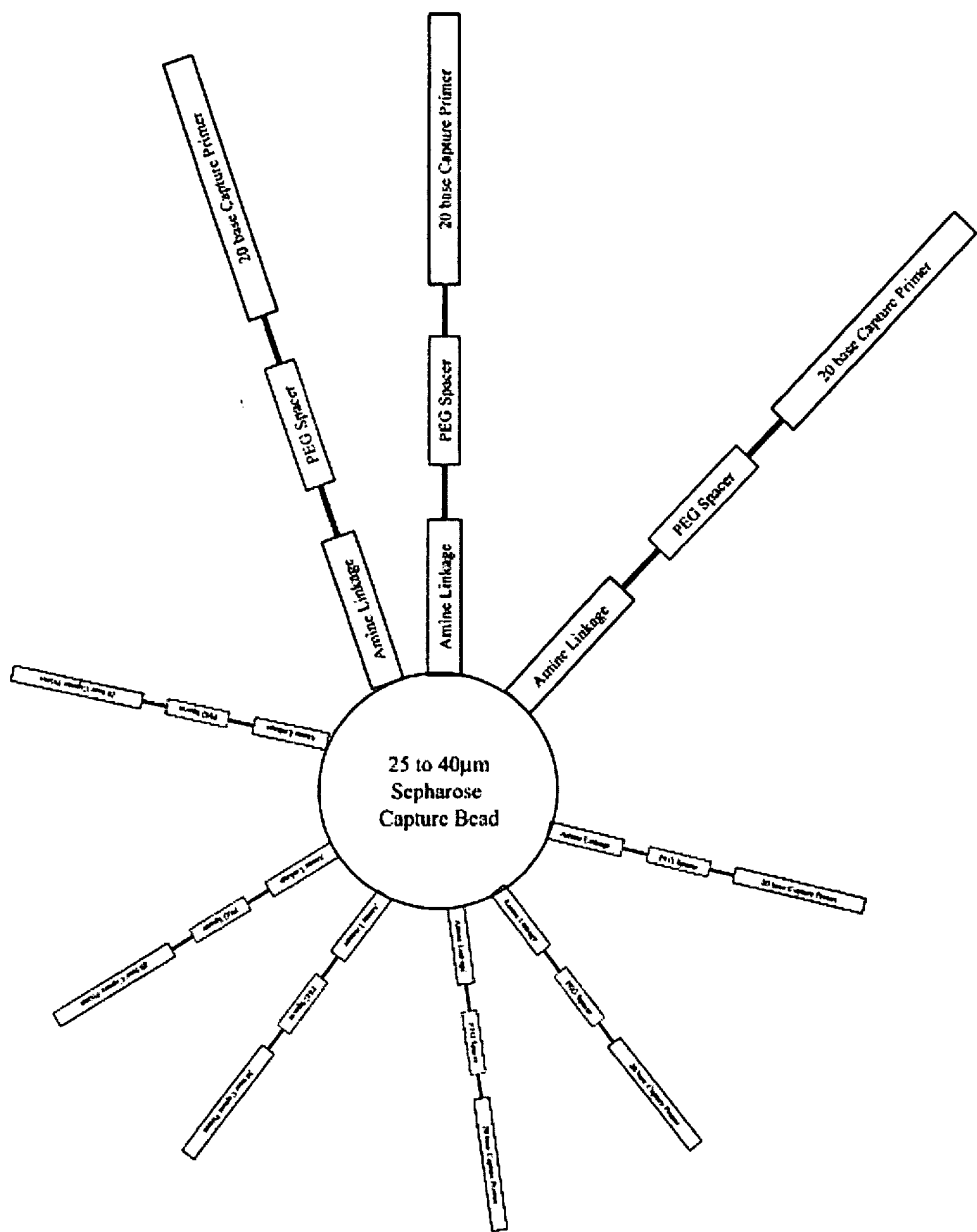


Figure 4

Possible double-stranded Genomic DNA Library Species:

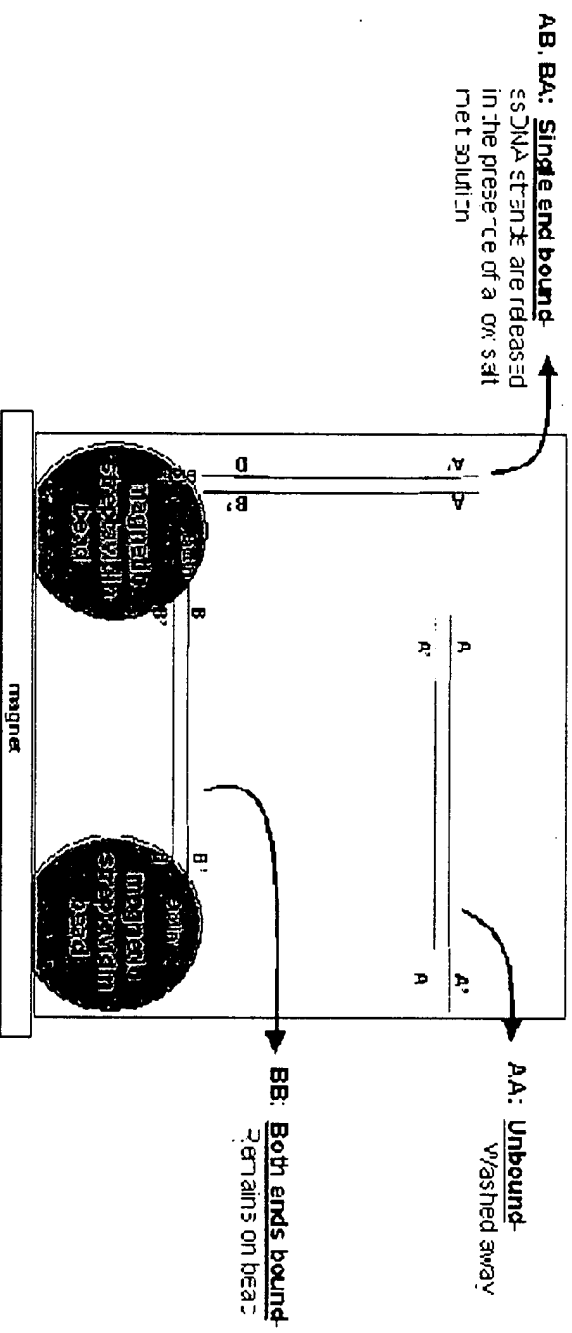
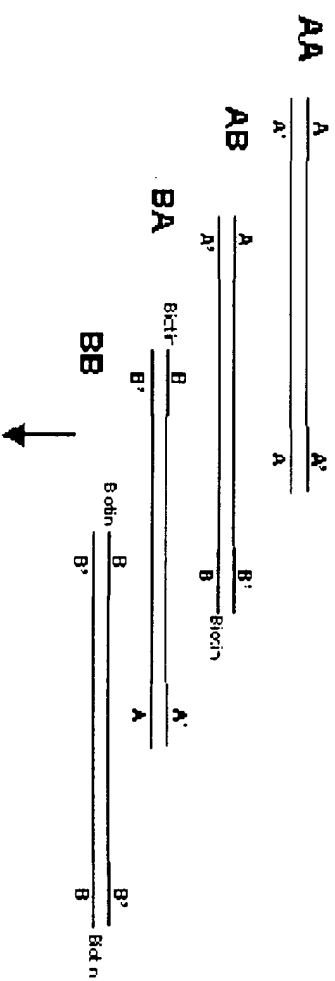


Figure 3

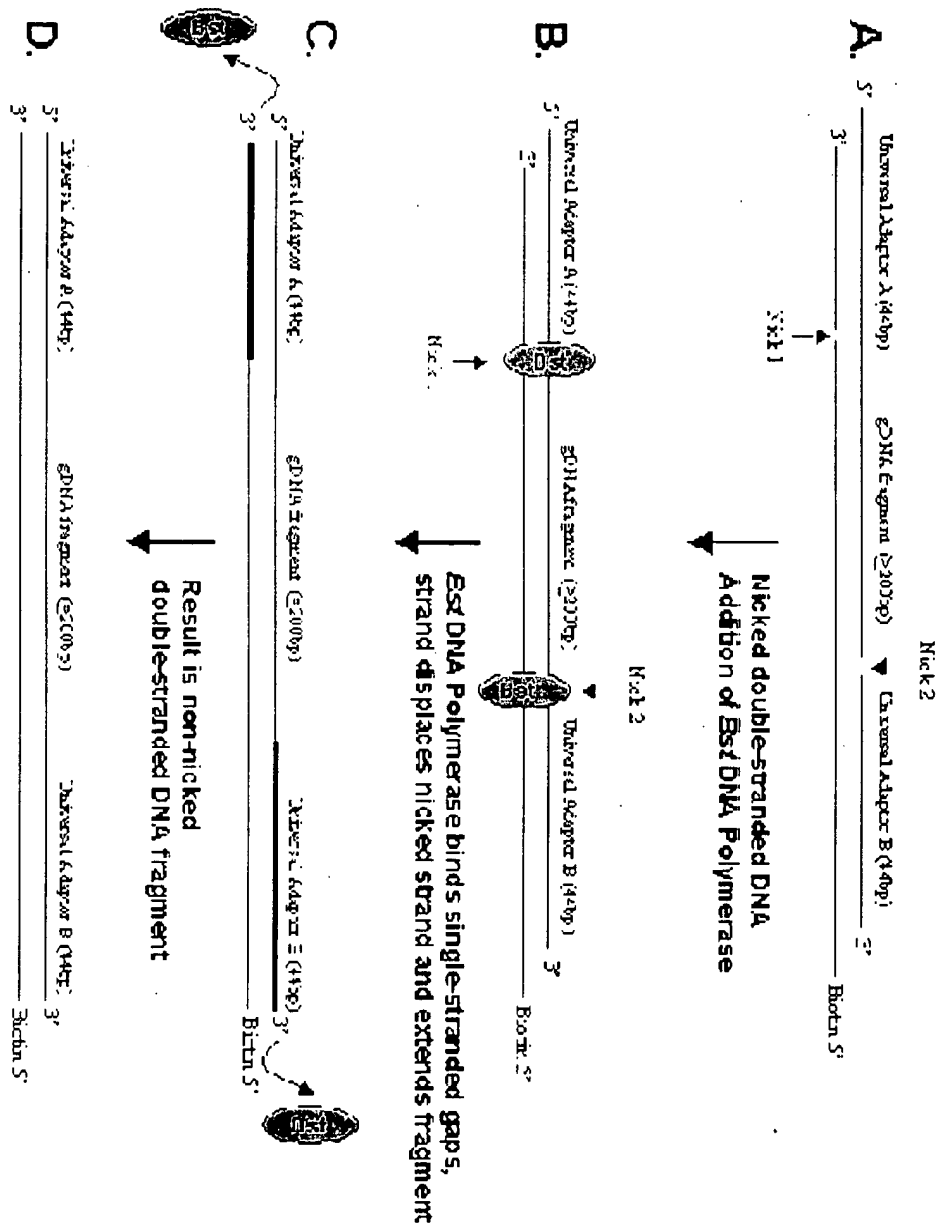


Figure 2A

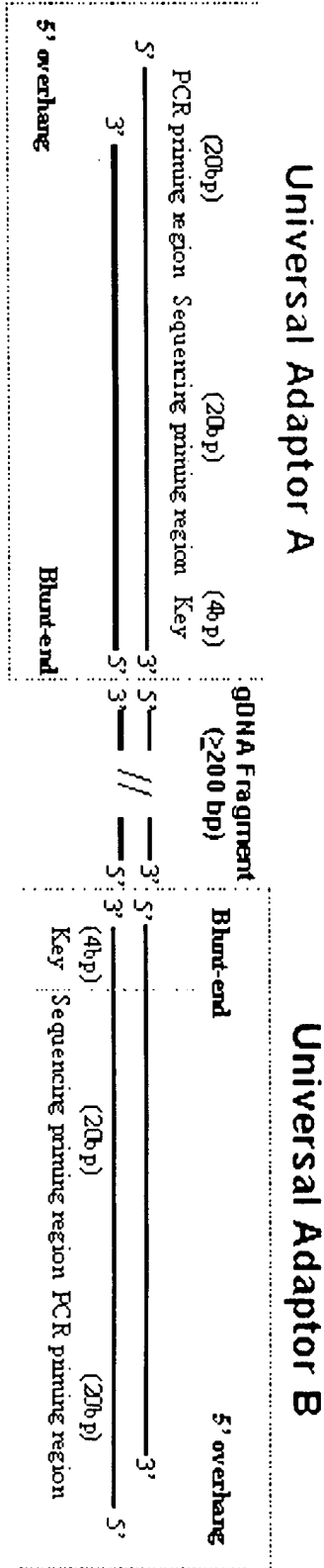
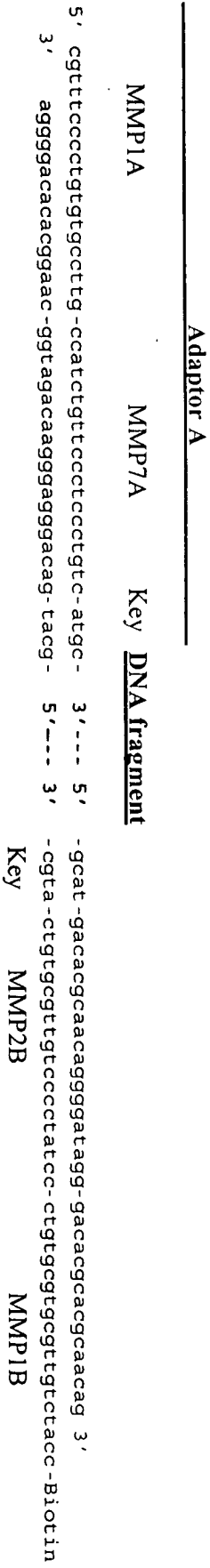
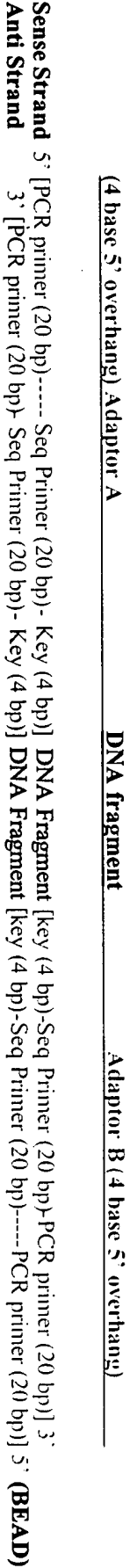


Figure 2B



Adaptor B

Figure 2C



The 454 Sequencing system

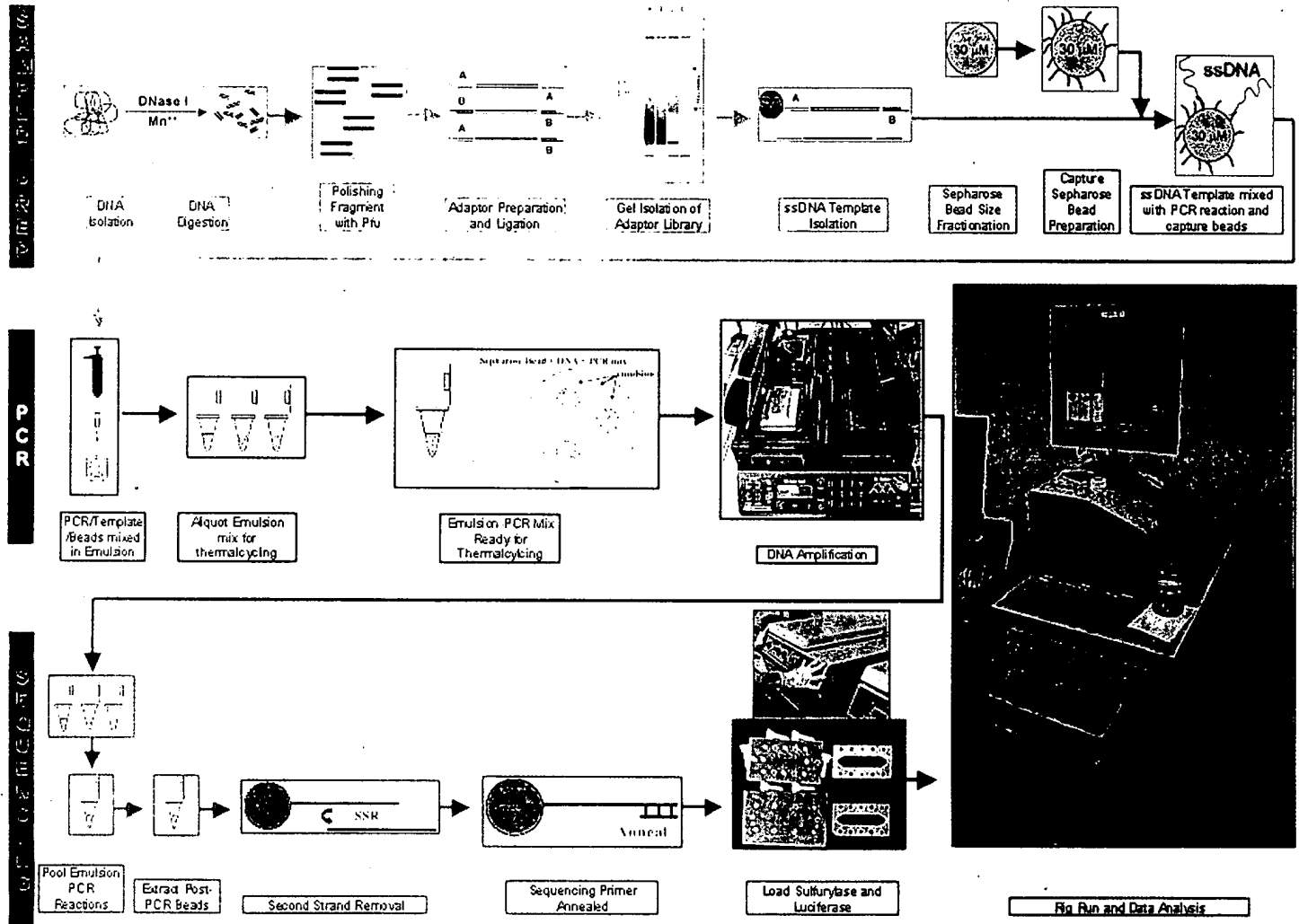


Figure 1 61

Figure 1F

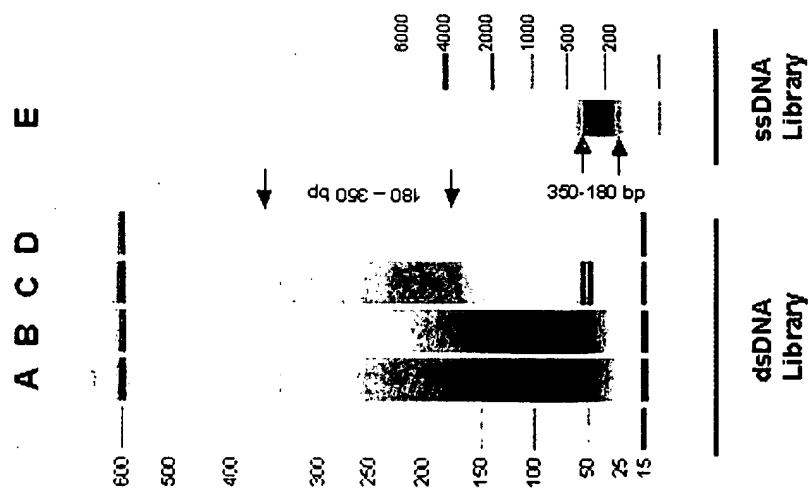


Figure 1A.

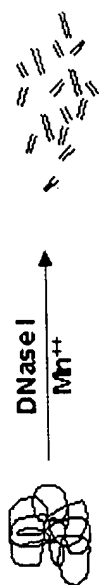


Figure 1B.

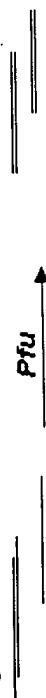


Figure 1C.



Figure 1D.

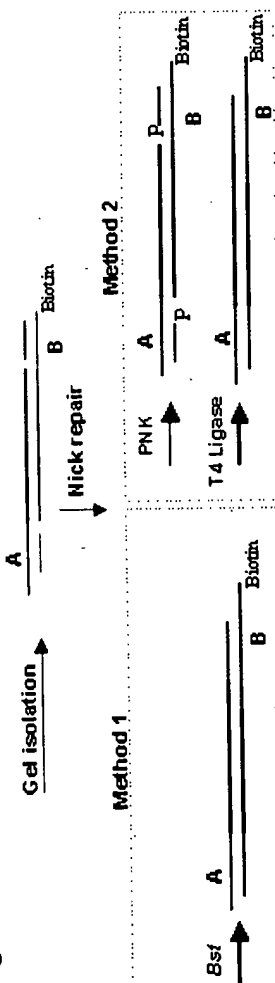


Figure 1E.

